Result No.

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Description

SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOULCE	RESULT 1 A56814 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM		44 44 55 44 44 45 44 45 44	33 35 40 40	470010 70 70 70			11 944
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KEYWORDS SOURCE ORGANISM

Yersinia Bacteria;

pestis
; Proteobacteria;

gamma

subdivision;

Enterobacteriaceae;

RESULT 3
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Yersinia M26405

2100 bp pestis lcrG,

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                                                                       0; IS1616; effector;
                                                                       IS1617; lcr;
transposase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.cc.uk DNA supplied by Dr. Andrey Karlyshev and Prof. Brendan Wren, [3]. Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, Keppel Street, London WCIE 7HT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beowulf Genomics
Details of Y. pestis sequencing at the Sanger Cen
on the World Wide Web.
(URL: http://www.sanger.ac.uk/Projects/Y_pestis/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretion; v antigen; virulence; ylp; yop; ysc. Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cannot be identified we choose the most upstream initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS are numbered using the following system eg YPPCP1.01c. YP (Y. pestis), PCP1 (plasmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 70305)
Baker, S.G. and Mungall, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-SEP-1999) Yersinia pestis sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strand).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Notes:
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                                                                                                                                                                                                                                                                                         putative insertion sequence ISI00, identical to corresponding CDS from Y.pestis KIM5 pCD1 (EMBL.AF053946, AF074612) (340 aa), fasta scores; opt: 2388 z-score: 3808.9 E(): 0, 100.0% identity in 340 aa overlap. Similar to many others e.g. TRA0_ECOLI (EMBL.X14793), istA, E.coli transposase for insertion sequence element IS21 (390 aa) (33.1% identity in 329 aa overlap). Contains Pfam match to entry pF00239 recombinase, Site-specific recombinases, score 25.70, E-value 4.8e-06. Contains probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="YPCD1.01"
88. .1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="IS100 element"
88. .1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Yersinia pestis"
/plasmid="pCD1"
/strain="CO-92 Biovar Orientalis"
/db_xref="taxon:632"
      translation="MVTFETVMEIKILHKQGMSSRAIARELGISRNTVKRYLQAKSEP/
                                                                                       /product="putative transposase"
/protein_id="CAB54878.1"
/db_xref="pID:e1549591"
                                                                                                                                                                            /transl_table=11
/label=YPCD1.01
                                                                                                                                                                                                                                                                 helix-turn-helix motif at aa 19-40 (Score 2045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="YPCD1.01, probable transposase, len: 340 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="YPCD1.01"
                                    /db_xref="PID:g5832424"
/db_xref="GI:5832424"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                        codon_start=1/
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                                                                                                                                                                                                                                                                    +6.15 SD)"
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/gene="YPCD1.04"
/note="YPCD1.04,
                                                         'partial
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/note="YPCD1.03c, probable transposase remnant, len: 83 aa; similar to several e.g. N-terminus of TRAO_ECOLI (EMBL:X14793), istA, E.coli transposase for insertion sequence element IS21 (390 aa), similarity is interrupted by the adjacent IS100 element. The remainder of this CDS is in YPCD1.97c. This region is also similar to TR:068707 (EMBL.AF053946, AF074612) y.pestis KIMS putative transposase in pCD1 (390 aa). Contains probable helix-turn-helix motif at aa 19-40 (Score 1833, +5.43 SD)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1110. .1889
/gene="YPCD1.02"
/note="YPCD1.02,
/gene="YPCD1.04"
2304. .2949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="YPCD1.02"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
complement(1956. 2204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -translation="MMELQHQRLMALAGQLQLESLISAAPALSQQAVDQEWSYMDFLE
HLLHEEKLARHQRKQAMYTRMAAFPAVKTFEEXDFTFARGAPKOLQSLKSLSFIERN
ENIVLLGEPSCYGKTHLAIAMGYEAVRAGIKVERTTAADLLLQLSTAQRGGRYKTTLGA
GYMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKRYEKSAMILTSNLPFGQWDQTFAGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         putative insertion sequence ISI00, identical to corresponding CDS from Y.pestis KINS pCD1 (EMBL:AF053946, COTTACE CONTROL (EMBL:AF053946, AF074612) (259 aa), fasta scores; opt: 1658 z-score: 2693.4 E(): 0, 100.0% identity in 259 aa overlap. Similar to many others e.g. ISTB_ECOLI (EMBL:X14793), istB, E.col.
                                                                /gene="YPCD1.03c"
2304. .2948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposase for insertion sequence element IS21 (265 aa) (47.4% identity in 249 aa overlap). Contains PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF00239 recombinase,
Site-specific recombinases, score 25.70, E-value 4.8e-06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDTLETCHRNAFRFFGGVPREVLYDNMKTVVLQRDAYQTGQHRFHPSLWQFGKEMGFS
PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRLRPMGITVDVETANRHGLRWLHDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKYTPRPAVASLLDEYRDYIRQRIADAHPYKIPATVIAREIRDQGYRGGMTILRAFIR
SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRSPLHVFVAVLGYSRMLYIEFTDNMR
                                                                                                                            complement(1956.
                                                                                                                                                              where noted"
                                                                                                                                                                                  (LMBL:AFUJJ946) from 46489 to 1955, and to Y.pestis KIM5
Plasmid PCD1 (EMBL:AF074612) from 59097 to 14563, except
                                                                                                                                                                                                                                                                                                                                ARKTRHKMVKLKPFMDYIDMRLAENVWNSEVILAEIKAM"
                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:g5832426"
/db_xref="GI:5832426"
/translation="mlsREDFYMIKQMRQQGAYIIDIATQVGCSERTVRRYLKYPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=YPCD1.03c
/protein_id="CAB54880.1"
/db_xref="pID:e1549593"
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                                                                                                                                                                                                                                                      1956. .46271
/note="identical to Y pestis KIM5 plasmid
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/db_xref="GI:5832425"
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1110. 1889
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/db_xref="PID:e1549592"
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/label=YPCD1.02
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                                                                                                                            .2204)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding protein"
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possible transposase remnant,

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Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                           646
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GTAAAAGAGTTCCTTGAATCATCGCCGAATACACAATGGGAATTGCGGGCGTTCATGGCA
                                                                 AATAGAGTAATTACTGATGATATCGAATTGCTCAAGAAAATCCTAGCTTATTTTCTACCC
                                                                                                                                                                                                                                  GATAAAAATATAGATATTTCCATTAAATATGATCCCAGAAAAGATTCGGAGGTTTTTGCC
                                                                                                                                                                                                                                                                                                AATAGAGTAATTACTGATGATATCGAAGTTGCTCAAGAAAATCCTAGCTTATTTTCTACCC
                                                                                                                                                                                                               GATAAAAATATAGATATTTCCATTAAATATGATCCCAGAAAAGATTCGGAGGTTTTTGCC
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/gene="YPCD1.05c"
complement(3014. 3406)
/gene="YPCD1.05c"
/gene="YPCD1.05c"
/gene="YPCD1.05c"
/note="YPCD1.05c", sycE, yerA, yopE targeting protein, len:
130 aa; identical to corresponding CDS from y.pestis KIM5
PCD1 (EMBL:AF053946, AF074612) (130 aa), fasta scores;
opt: 861 z-score: 1608.5 E(): 0, 100.0% identity in 130 aa
overlap and to YERA_YERPE (EMBL:M34279) from Y.pestis
plasmid pYV019. Highly similar to TR:Q56910 (EMBL:218539),
sycE, from Yersinia enterocolitica (130 aa) (99.2%
identity in 130 aa overlap) and YERA_YEREN (EMBL:M34278),
yerE, also from Y.enterocolitica (130 aa) (98.5% identity
in 130 aa overlap). Similar to TR:Q51448 (EMBL:M34278),
ORF1, Pseudomonas aeruginosa exoenzyme S ORF1 (116 aa)
(44.3% identity in 115 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative yopE cl
/protein_id="CAB54882.1"
/db_xref="PID: CAB54955"
/db_xref="PID: 95832428"
/db_xref="GI: 5832428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="YPCD1.06"
3600. .4250
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QILMFTLPSLDNNDEKETLLSHNIFSQDILKPILSWDEVGGHPVLMNRQPLNSLDNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2304. .2982
_note="similar to E.agglomerans IS 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="hreglhvnhkrvyrlyhlsglgvkrrrrrkglaterlpllrpaa
pnlfysmdfymblatgrrikglfcvddytkeclfvfyafglsgovynfrildstalfr
gypatirtogopeffcraldomafethyelrilgfkerfyngfiesfmarfroeche
hwfsdvsharktisewrodynecrphstlnyofpsefaaawrkgnsdsegsditk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=YPCD1.04
/protein_id="CAB54881.1"
/db_xref="PID:e1549594"
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/db_xref="GI:5832427"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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IS 1222 ORFB (276 aa). Truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                       21955
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                                                                                                                                                                                                                                                                                                                                                                                                                   GATGACACGTCTGGTAAATGA 21935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGACTTGGTTAGCCAAAAAACAACTCAGCTGTCTGATATTACATCACGTTTTAATTCA 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGATAATGAATTATCTCACTTTGCCACCTGCTCGGATAAGTCCAGGCCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAAGTGAGAATAAAAGAACCGGGGCGTTGGGTAATCTGAAAAACTCATACTCTTATAAT 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATACAGATGAAGATTTTTAAAGCCAGCGCAGAGTACAAAATTCTCGAGAAAATGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTCAATGAATCATCATGGTGATGCCCGTAGCAAGTTGCGTGAAGAATTAGCTGAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGACACGTCTGGTAAATGA 1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTATTGAAGCACTGAACCGTTTCATTCAGAAATATGATTCAGTGATGCAACGTCTGCTA 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGATAATAATGAATTATCTCACTTTGCCACCACCTGCTCGGATAAGTCCAGGCCGCTC
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                                                                                                                                                                                                                                                                            Yersinia pe
AF053946
92996222
AF053946.1
                           Hu,P., Elliott,J., McCready,P., Kobayashi,A., Carrano,A.V., Brul Direct Submission
                                                                                                                                    Hu,P., Elliott,J., McCready,P., Skowronski,E., (Kobayashi,A., Brubaker,R.R. and Garcia,E. Structural organization of virulence-associated
               Submitted (16-MAR-1998)
                                                                                                       J. Bacteriol. 180 (19),
                                                                                                                                                                                                                                Yersinia
 Livermore National Lab,
                                                                                          98422474
                                                                                                                        Yersinia pestis
                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision;
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                                                                                                                                                                                                     Yersinia.
                                                                          (bases 1 to 70504)
                                                                                                                                                                                     (bases 1 to 70504)
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                                          Brubaker, R. and
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                                                            Skowronski, E.,
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complement(6937. .7200)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mkyklnvllaeialigtgnhyheeanciaewlhlkgeeeavoli
RLSSLMNRGDYASALQQGNKLAYPDLEPWLALCEYRLGLGSALESRLNRLARSQDPRI
QTFVNGMREQLKT"
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/db_xref="GI:2996226"
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/db_xref="PID:g2996225"
/db_xref="GI:2996225"
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Pred. No. 3.5e
O; Mismatches
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3.5e-204;
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Yersinia
AF074612
g3822037
                                                                                                                                                                                                   Unique
pCD1.
                                                                                                                                                                                                                Submitted (25-JUN-1998) Microbiology and Immunology, University of Kentucky, MS415 Medical Center, Lexington, KY 40536-0084, USA Unique identifiers, starting at Y0001, are assigned to each gene o
                                                                                                                                                                                                                                                                                                                                                      DNA sequencing and analysis of the low-Ca2+-response of Yersinia pestis KIM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia pestis
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                              Blattner, F.R.
                                                                                                                                                                                                                                                                                              Perry,R.D.,
                                                                                                                                                                                                                                                                                                                              98427122
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                                                                                                                                                                                                                                                                Submission
                                                                                                                                                                                                                                                                                                                                           Immun. 66 (10),
                                                            /gene="Y057..368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70559 bp
pestis plasmid
/gene="Y0001"
/note="0103; 43 pct identical (0 gaps) to 100
an approx. 200 aa protein GENPEPT: gi|537126,
Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pestis.
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                       /organism="Yersinia
/plasmid="pCD1"
                                                                                                     /db_xref="taxon:632"
                                                                                                                         /strain="KIM5"
                                                                                                                                                                                                                                                                                             Straley, S.C.,
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                                                                              "Y0001"
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pCD1,
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                                                                                                                                                                                                                                                                                                                                           (1998)
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                                                                                                                                                                                                                                                                                             Rose, D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                      plasmid
                 orf_o198
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                                                                                                         rep_origin
                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
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/db_xref="GI:3822042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown"
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/translation="MHQQSRGAAGSRTLSLLMRQSGYINVVRWLARRLMRECGLASRQP
complement(3427. .3645)
/gene="Y0006"
complement(3427. .3645)
/gene="Y0006"
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/translation="mdtkllQhtpigtmydyrpvntksggkrlrrcpdfvihyrmdll
vnagipvrtvnsfkalhdkviivdgkntQmgsfnfsQaavQsnsenvliiwgdftvvQ
aylQywqsrnnkgtdwrssy"
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                                                                                                                                                   GLKRARARRDVDRTRRDIEAIVNRQLTREIAEGRFVGNLDAVRREKARRVKERMLMSF
                                                                                                                                                                  /translation="MTNHQALFTHHYRQVKNPNPEETPREGKKTLPECRKLMAKAEGF
TSRPDFSMHYAFARSLSLRHRWPLLERRAIDALLGGKCFHYDFDLANRIORSITMLAI
ECCLATESKSGNLSITRATRALFELSELGLITYQTEVPPQIGCNIPTDITETPALFSA
LDVSDVAVAAARRSRVEWENQQREKQRLPRLEMDELIAKAWRFVRERFRSYQTERKAH
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FIQNDLKNELLQLCEDSGLTQTEMIERWIQREKAARTNAA"
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|667. .1741
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                                                                                     /note="oriR"
                                                                                                                                                                                                                                                                                                                                                                                     'gene="repA"
                                                                                                                                                                                                                                                                                                                                                                                                                               note="Y0005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="repA"
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db_xref="PID:g3822039"
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/gene="Y0008"
4758. 5100
9858. .10064
/gene="Y0012"
9858. .10064
/gene="Y0012"
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ALSNLFGAKPQTELPLAWKGBPLSGARDLEGMRVAETDKFABGESHTSIIFRKOKGIF
VAKIERSIAEGHLFAELEAYKHIYKTAGKHPNLANVHGMAVVPYGNRKEEALLMDEVD
GWRCSDTLRTLADSWKQGKINSEAYWGTIKFIAHRLLDVTHHLAKAGVVHNDIKPGNV
VFDRASGEPVVIDLGHRSGEOPKGFTESFKAPELGFUNGASEKSDVFLVYSTLH
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ADSRPDSNEARLHEFLSDGTIDEESAKQILKOTLTGEMSPLSTDVRRITPKKLRELSD
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KHLETLLEVLYTLSQGGQPVSSETYGFLNRITEAKTTLSQQLNGHSFNSLIKATGAN
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VEMDLORSSSECGIFSLALKKLYIERDSLLKIHEDNIKGILSGENPLPHOKLDPYL
VEMDLORSSSECGIFSLALKKLYIERDSLLKIHEDNIKGILSGENPLPHOKLDPYL
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/protein_id="AAC69765.1"
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/db_xref="GI:3822045"
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deilnrltilgeilgesgebarsaasolffcysinalnkdgpcfamseelgliafkhl
sldelnvenvskeianfydmlslvslpaetapsysiysig"
                                                                                                                                                        KRIAEYKTLLKV"
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/note="Y0010"
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residues of an approx.
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/protein_id="AAC69763.1"
/db_xref="PID:g3822043"
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                                                                                                                                                                                            PVTFYKHTQGKKRLNEYLNTNPQGVGTVVNKKNETIVNRFDNNKSIVDGKELSVSVHK
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/transl_table=11
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/note="Y0009"
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/db_xref="PID:93822044"
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/gene="Y0008"
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/translation="MRSPLAYGCSVYTVNVVTQLHNDIHKSAYKHKRLYHVLTGQASS
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px. 104 aa protein GENPEPT: g
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45 pct identical (0 gaps) to

68 residues

of, an

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Query Match
Best Local Similarity 99.9
Matches 980; Conservative
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                                                             GGAAGTGAGAATAAAAGAACCGGGGGCGTTGGGTAATCTGAAAAAACTCATACTCTTATAAT
                                                                                                                                      CAAACCACCATTCAGGTGGATGGGAGCGAGAAAAAATAGTCTCGATAAAGGACTTTCTT
                                                                                                                                                                                                                    TATACAGATGAAGAGATTTTTAAAGCCAGCGCAGAGTACAAAATTCTCGAGAAAATGCCT
                                                                                                                                                                                                                                                                                                                                                                           ACCGCCGAATTAAAGATTTATTCAGTTATTCAAGCCGAAATTAATAAGCATCTGTCTAGT
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                                      GGAAGTGAGAATAAAAGAACCGGGGCGTTGGGTAATCTGAAAAACTCATACTCTTATAAT
                                                                                                                  CAAACCACCATTCAGGTGGATGGGAGCGAGAAAAAAATAGTCTCGATAAAGGACTTTCTT
                                                                                                                                                                                               TATACAGATGAAGAGATTTTTAAAGCCAGCGCAGAGTACAAAATTCTCGAGAAAATGCCT
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/note="Y0013"
10347. .11753
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/gene="yopH"
/codon_start=1
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/codon_start=1
/transl_table=11
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                                                                                          TGGAACAACTTACTGGTCATGGTTCTTCAGTTTTAGAAGAATTGGTTCAGTTAGTCAAAG
                                                                                                        TGGAACAACTTACTGGTCATGGTTCTTCAGTTTTAGAAGAATTGGTTCAGTTAGTCAAAG
                                                                                                                                                     TCATTAGAGCCTACGAACAAAACCCCACAACATTTATTGAGGATCTAGAAAAAGTTAGGG
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ATAGAGTAATTACTGATGATATCGAATTGCTCAAGAAAATCCTAGCTTATTTTCTACCCG
                            ATAAAAATATAGATATTTCCATTAAATATGATCCCAGAAAAGATTCGGAGGTTTTTGCCA
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/TRANSLATION="MSEFIRAYEONPOHFIEDLEKVRVEQLIGHGSSVLEELVQLVKD
KNIDISIKVDPRKDSEVFANRVITDDIELKKILAYFLPEDAILKGGHYDNQLQNGIK
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AELTAELKIYSVIQAEINKHLSSSGTINIHDKSINLMKYGYTDEEIFKASAEYKI
LEKMPQTTIQVDGSEKKIVSIKDFLGSENKRYGALGNLKNSYSYNKDNNELSHFATTC
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Titball, R.W., Williamson, E.D., Lear Bennett and Alice, M. WACCINES FOR PLAGUE Patent: WO 9628551-A 1 19-SEP-1996;
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                                                                            TCAATGAATCATCATGGTGATGCCCGTAGCAAGTTGCGTGAAGAATTAGCTGAGCTTACC
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Titball,R.W., Williamson,E.D., Lear
Bennett and Alice,M.
VACCINES FOR PLAGUE
Patent: WO 9628551-A 3 19-SEP-1996;
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V antigen.
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Direct Submission
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Passive immunity to infection with Yersinia anti-recombinant V antigen is dependent on F
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/codon_start=1
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/product="V antigen"
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/db_xref="PID:g1405835"
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                                                                                                                 GAAAGTGAGAAAAAAAAGAACCGGGGCGTTGGGTAATCTGAAAGACTCATACTCTTATAAT
                                                                                                                                                                                               CAAACCACCATTCAGGAAGGTGAGACCGAAAAAAAAAATAGTCTCGATAAAGAACTTTCTT
                                                                                                                                                                                                                                                                          TATACAGATGAAGAGTTTTTTAAAGCCAGTGCAGAGTACAAAATTCTCGAGAAAATGCCT
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SRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK"
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No. 2.9e-199;
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241. 246
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252. 258
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                                                                                                                  AGTGGCACCATAAATATCCATGATAAATCCATTAATCTCATGGATAAAAATTTATATGGT 1185
                                                                                                                                                                                                             GATTCAATGAATCATCGTGGTGATGCCCGTAGCAAGTTGCGTGAAGAATTAGCTGAGCTT 1032
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CAAACCACCATTCAGGAAGGTGAGACCGAAAAAAAAATAGTCTCGATAAAGAACTTTCTT
                      CAAACCACCATTCAGGTGGATGGGAGCGAGAAAAAAATAGTCTCGATAAAGGACTTTCTT 1305
                                                            TATACAGATGAAGAGATTTTTAAAGCCAGCGCAGAGTACAAAATTCTCGAGAAAATGCCT
                                                                                                    GGTGGCACCATAAATATCCATGATAAATCAATTAATCTCATGGATAAAAATTTATATGGT
                                                                                                                                                                       ACCGCCGAATTAAAGATTTATTCAGTTATTCAAGCCGAAATTAATAAGCATCTGTCTAGT 1125
                                                                                                                                                        ACCGCCGAATTAAAAATTTATTCAGTTATTCAAGCTGAAATTAATAAGCATCTGTCGAGT 1092
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a 450 c
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SRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK"
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                                            Wattiau, P., Bernier, B., Deslee, P., Michiels, T. and Cornelis, Individual chaperones required for Yop secretion by Yersinia Proc. Natl. Acad. Sci. U.S.A. 91 (22), 10493-10497 (1994)
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Yersinia enterocolitica plasmid pYVe227, complete sequence.
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AF080155 AF022645 AF050104 AF054977 AF033863 U02499 U08019 U21297
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J. Bacteriol. 171 (1), 254
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/translation-"MINTTFTELLQKIASHFGLDKLSQDEYGLCELILNDRVVIMLRA DEILNRLTLLGPILGFSGPEARSTASQLEFCYSINALNKDGPCTAWSEELGLIAFKHL SLGELNVERUSKEIANFYDWLSLYSLPAETQQELPPHTQSTQSTQSTQSVKWG" 20914280 /gene="yopo"	KLRPSEYSIHAKMLDISRLY"  1616. 2083 /note="ORF155" /codon_start=1 /trans1_table=11 /product="unknown" /protein_id="AAD16802.1" /db_xref="PID:94324325" /db_xref="GI:4324325"	/ COGON_SEATE=1 / trans_1_table=11 / trans_1_table=11 / product="unknown" / protein_id="AAD1801.1" / db_xref="ptD: 94324324" / db_xref="gtI: 4324324" / db_xref="GI: 4324324" / trans_lation="MRVVIYQGQYGIFKKNGLDLSMPAIQTCLGLYALSDQHDYLLCA / trans_lation="MRVVIYQGQYGIFKKNGLDLSMPAIQTCLGLYALSDQHDYLLCA / trans_lation="MRVVIYQGQYGIFKKNGLDLSMPAIQTCLGLYALSDQHDYLLCA FMKSHGALAQYSNQYYSGVFPETENFHYQKGCGITKGQNPRDFLGGSPQAMNLAKQRI FMKSHGALAQYSNQYYSGVFPETENFHYQKGCGITKGQNPRDFLGGSPQAMNLAKQRI	> 0.11	/organism="Yersinia enterocolitica" /strain="W22703" /serotype="0:9" /db_xref="taxon:630" /plasmid="pyYe227"	gi:3603357 gi:497215 I	on May 18, 1999 this sequence version replaced gi:3411136 on May 18, 1999 this sequence version replaced gi:3411136	. 2 = 4	Unpublished 12 (bases I to 69673) 12 inarte,M., Lambermont,I., Kerbourch,C. and Cornelis,G.R. Direct Submission	9819073 11 (bases 1 to 69673) 1. Iriarte,M., Lambermont,I., Kerbourch,C. and Cornelis,G.R. Detailed genetic map of the pYVe227 plasmid of Yersinia enterocolitica serotype 0:9	TyeA, a protein involved in control of Yop release and in translocation of Yersinia Yop effectors  EMBO J. 17 (7), 1907-1918 (1998)	Mol. Microbiol. 27 (2), 425-436 (1998) 98143428 10 (bases 22612 to 22890) 11 intarte,M., Sory,M.P., Boland, A., Boyd, A.P., Mills, S.D.,	9 (bases 18681 to 18968) 9 (bases 18681 to 18968) Boyd.A.P., Sory.M.P., Iriarte,M. and Cornelis,G.R. Heparin interferes with translocation of Yop proteins into HeLa cells and binds to LcrG, a regulatory component of the Yersinia Yop	8 (bases 53135 to 53497) 8 (bases 53135 to 53497) 8 (bases 53135 to 53497) Stainier, I., Iriarte, M. and Cornelis, G.R. YSCM1 and YSCM2, two Yersinia enterocolitica proteins causing downregulation of yop transcription Mol. Microbiol. 26 (4), 833-843 (1997)	VirG, a Yersinia enterocolitica lipoprotein involved in Ca2+ dependency, is related to exsB of Pseudomonas aeruginosa J. Bacteriol. 177 (15), 4230-4237 (1995) 9535364
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/product="YopQ" /protein_id="AAD16807.1" /db_xref="pID:94324330" /db_xref="GI:4324330" /db_xref="GI:4324330" /translation="MFIKDAYNMRALCTALEQSAPDTIINTSKEENNSYYCATAHLLR	NVLKADKMDLREAEGFLSQGYGAALGAAGAGTTCYNSNGSAGASLGVGKVADAWVEDINYTMYTDVQISEKTDTFLQTDNVAALKQGTSGYKVQTSTQTGNKHQYQTR VVSSANKVNLKFEEAQPVLEDQLAKSIANIL"  complement(73707918)  /gene="yop0"  complement(73707918)  /gene="yop0"  /codon_start=1  /trans1_table=11	/gene="ylpA" /codon_start=1 /transl_table=11 /transl_table=11 /product="lipoprotein ylpA" /protein_id="AAD16806.1" /db_xref="PID:94324329" /db_xref="PID:94324329" /translation="MEDDMKRNMKLIAITAVLSSVLVLSGCGAMSTAIKKRNLEVKTO MSETIWLEPSSQKTVYLQIKNTSDKNMLGLAPKITKAVQDKGYTVTSSPEDAHYWIQA	<pre>complement(61516900) /gene="ylpA" complement(61516900)</pre>	FHKNYSRLDIEVMPALVIQANNKYPEMNLNFVTSPQDLSIEIKNVIENGVGSSRFIIN MGEGGIHFSVIDYKHINGKTSLILFEPVNFNSMGPAILAISTKTAIERYQLDCHFSM VEMDIQRSSSEGGIFSLALAKKLYTERDSLLKIHEDNIKGILSDSENPLPHNKLDPYL PVTFYKHTQGKKRLNEYLNTNPQGVGTVVNKKNETIFNRFDNNKSIIDGKELSVSVHK KRIABYKTLLKV"	/Production of the control of the co	/COGOT_START=1 /transl_table=11 /nrodict="Yon offector Yong"	/gene="yopp" 47615627 /gene="yopp"	/db_xref="GI:4324327" /translation="MLSIRKNECPCWTLNNGLPVICSGELAINEGKFVGINNYSALYR IMNLGVLVRVLPVCSGFTHQRLNVLLQGTVYPEYKIHTAVNSLNKDK" 47615627	/codon_start=1 /trans1_table=11 /product="unknown" /protein_id="AAD16804.1" /db_xref="PID:g4324327"	RSGSWADVAKGSLGREDSIKTVYKEGIEGIIAIHKQMMAAHAAITLGEVSEEIDUMKN FTADSIPLLIRLGRSSLIDEHLVEQREKLRELTTIAERLNRLEREWM" 4485. 4760 /note="ORF91A; unknown function"	GFEKUPELK PROGLEK ITSEPAH YMLENGY PLHKPGLAG VETAYIK ITU LGVSAUS RPDSNEARLHEFLSDGT IDEESAKO ILKOTLTGENGLAG VETAYIK ITU LGVSAUS RTLLSSAATKOLDMGVVLSDLDTMLVTLDKAEREGGVDKDQLKSFNSLILKTYSVIEDY VKGREGDTKSSSAEVSPYHRSNFMLSIAEPSLQRIQKHLDQTHSFSDIGSLVRAHKHL ETLLEVLVTLSPQGQPVSSETYSFLMRLABAKVTLSQQLDTLQQQESAKAQLSILIN	VLRIMPHSGFSLFREGYGK IFSGKMENFSTARNITTETHÄAGKTTSGELRSDIPNALS NLFGAKPQTELPLGWKGK PLSGAPDLEGMRVAETDKFAEGESHI SI IETK DNORLVAK IERSI AEGHLFAELEAYKH IYKTAGKHPNLANVHCWAVVPYGNRKEEALLANDEVDGWR CSDTLRSLADSWKQGK INSEAYWGT IKF I AHRLLDVTNHLAKAG I VHNDI K PGNVVFD RASGEPVVI DUGLHSRSGEQPKGFTESFKAP ELGYGNLGASEKSDV FLVVSTLLHG I E	/product="protein kinase ropo" /protein_id="nAD16803.1" /db_xref="PID:94324326" /db_xref="Gi.4324326" /translation="MKIMGTMPPSISLAKAHERISOHWQNPVGELNIGGKRYRIIDNQ	2091 .4280 /gene="yopo" /codon_start=1 /transc1 +ahie=1

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Submitted (22-MAR-1996) A.
University of Wuerzburg, Jo
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/product="V antigen"
/protein_id="CAA65593.1"
/db_xref="plD:q420588"
/db_xref="plD:q4205831"
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/db_xref="SPTREMBL:Q55882"
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/db_xref="SPTREMBL:Q558882"
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DISIXTDPQXDSEV*MIRAYEDDIELLKKILAYFLPEDAILKGGHYDNQLQNGIKRVK
DISIXTDPQXDSEV*MIRAYEDDIELLKKILAYFLPEDAILKGGHYDNQLQNGIKRVK

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TAELKISVIQABINKHLSNSDTINIHGKSINLMKNLYGYTDEBIFKASAEYKILEK
MPQTTIKEGETEKKIVSISIKNFLESENKRTGALGNLKDSYSYNKDNNELSHLGTTCSDK
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/strain="Y-96-p"
/db_xref="taxon:34055"
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/db_xref="taxon:630"
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Josef-Schneider Strasse 2, 97080
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Yersinia enterocolitica
Bacteria; Proteobacteria;
Roggenkamp, A., Heesemann, J.
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                  AATAGAGTAATTACTGATGATATCGAAITGCTCAAGAAAATCCTAGCTTATTTTCTACCC
ACCGCCGAATTAAAGATTTATTCAGTTATTCAAGCCGAAATTAATAAGCATCTGTCTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Passive immunity to infection with Yersinia anti-recombinant V antigen is dependent on [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roggenkamp, A.
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1. .975
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1. .975
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/strain="Y-108-P"
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Compugen Ltd
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Searched: Scoring table: IDENTITY\_NUC 3032314 seqs, 1171202697 residues ATGGGCCATCATCATCA.....ATGACACGTCTGGTAAATGA 1566

Database

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## SUMMARIES

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ATGAAACAAGGTTGTTTATTAAAAATGAATATAAATGAAATTAATGAAA 419
                                                                                                                                                                                                                                GTTATTCAAGCCGAAATTAATAAGCATCTGTCTAGTAGTGGCACCATAAATATCCATGAT 1149
                                                                                                                                                                                                                                                                                                         GCCCGTAGCAAGTTGCGTGAAGAATTAGCTGAGCTTACCGCCGAATTAAAGATTTATTCA 1089
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                                                                                                               GCCAGCGCAGAGTACAAAATTCTCGAGAAAATGCCTCAAACCACCATTCAGGTGGATGGG 1269
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                                   AGCGAGAAAAAATAGTCTCGATAAAGGACTTTCTTGGAAGTGAGAATA 1318
                                                                                                                                                    University of Tsukuba
University of Tsukuba, Ibaraki 305, Japan
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium' discoideum cDNA proj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M. Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Madda, M., Takeuchi, T., Ochiai, H. and Tanaka, Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU038989 579 bp mRNA EST 29-MAR-1999
AU038989 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSM246, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Hideko Urushihara
Institute of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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/clone="SSM246"
/clone_lib="Dictyostelium discoideum
/clone_lib="Dictyostelium discoideum
/dev_stage="slug"
/dev_stage="slug"
31 c 52 g 210 t
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/strain="AX4"
/db_xref="taxon:44689"
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Mismatches 192;
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                    ATCCATGATAAATCCATTAATCTCATGGATAAAAATTTATATGGTTATACAGA 1193
                                                                                           ATTTATTCAGTTATTCAAGCCGAAATTAATAAGCATCTGTCTAGTAGTGGCACCATAAAT 1140
ATTTATTCAGTCATTTCAAAGGTATTGAATGAGCATCTGCCAGGTGCTGGAATGTTGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 1655
High quality sequence stops: 342
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 1655
Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST Project Unpublished (1995)
On Apr 14, 1993 this sequent
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/clone="IMAGE:240523"
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/db_xref="GDB:3789656"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares fetal liver spleen 1NFLS'
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                                                                                                                                                             2.6%;
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                                                                                                                                          Score 41; DB Pred. No. 2.2; 0; Mismatches
                                                                                                                                                         DB
2.2;
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                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 394)

Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Hölder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E. Current status of the Plasmodium falciparum genome project
                                                                                                                                                                                                                                                                                               N97614 394 bp mRNA 1054C3 czapPFDd2.1, Debopam C clone PF1054C, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshino,R., Morio,T. and Tanaka,Y.
Developmental cDNA in Dictyostelium discoideum
Unpublished (1997)
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C91275 Dictyostelium discoideum SS
                                                                                                                                                                                                                                                                                  N97614
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Dictyostelium discoideum
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May 5, 1995 this sequence version replaced gi:798390
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                                    Biochem. Parasitol.
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/dev_stage="slug"
86 c 56 g 146 t
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/strain="AX4"
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/map="17q21"
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C84881.1
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Department of Molecular Biolo
University of Central Florida
Orlando, FL 32816-2360
Eukaryota; Dictyosteliida; Dictyostelium
1 (bases 1 to 510)
                                     Dictyostelium discoideum
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Seq primer: T3.
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Fax: 407 384 3095
                                                          Dictyostelium discoideum.
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/lab_host="E. coli XI-1 blue"
/lab_host="E. coli XI-1 blue"
/note="vector: Lambda ZAP II: Site_1: EcoR I: Site_2: Xho
I: PolyA+ RNA, from asynchronous blood stage parasites of
the Dd2 isolate cultured in vitro, was reverse transcribed
using an oligo dT Xho I primer. Second strand was
prepared using RNase H and DNA polymerase I. EcoR I
adapters were ligated to the cDNA, and it was digested
with Xho I. Prepared fragments were ligated into EcoR I +
Xho I digested lambda ZAP II vector."

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nt of Molecular Biology
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/db_xref="taxon:5833"
                                                                                                    GI:2865028
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AUTHORS

Morio

T., Urushihara, H., Saito, T.,

Ugawa,Y.,

Mizuno, H.,

Yoshida, M.,

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BASE COUNT
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                                                                                                                                                                                                         Unpublished On Sep 12, 1
                                                                                                                                                                                                                     Sexual-cDNA in CSM
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                        C22922 1107 bp
C22922 Dictyostelium d
discoideum cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cl
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University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
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99156227
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                                                                                                                                                   University of Tsukuba
                                                                                                                                                                              Contact: Hideko Urushihara
                                                                                                                                                                                                                                                 Shimizu, H. and Urushihara, H
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                                                                                                         Ten-nodai, Tsukuba, Ibaraki 305, d402hu@sakura.cc.tsukuba.ac.jp.
Location/Qualifiers
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/db_xref="taxon:44689"
/clone="SSD366"
/clone="SSD366"
/clone="Stypace"
/clone="b"Dictyostelium discoideum
/clone_lib="Dictyostelium discoideum
/clov_stage="slug"
/dev_stage="slug"
79 c 53 g 190 t 1 ot
                                     /organism="Dictyostelium
/strain="KAX3"
/db_xref="taxon:44689"
/clone="FC-AM03"
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Local Similarity 47.0%;
tes 119; Conserva+***
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
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g5851554
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                                                                                                                                                                                                                                                                                                      Pharmaceuticals, Inc. 4633 World Parkway Circle, St. Tel: 877-577-2733
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701932008 A. thaliana, mi
701932008, mRNA sequence.
                                                                                                                                                                                                                            Email: service@genomesystems.com
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            Genome Systems, Inc., a wholly owned subsidiary of Incyte
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: David Smoller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
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/clone_lib="A. thaliana, mixed source"
/note="This sequence was obtained from
with a PCR product of the target gene."
118 c 130 g 98 t
                                                                                                                                                  /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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                                                                                                   /clone="701932008"
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                               ATAAGTATGTATAATATACATATTTATGATATGTAAATATTTATGTGTTTATATACAT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL121551 489 bp mRNA
DKFZp762L088_r1 762 (synonym: h
DKFZp762L088 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                     This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubne Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                       Berlin-Charlottenburg, GERMANY;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              No si sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequenced by MediGenomix within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Ottenwaelder B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ottenwaelder,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 489)
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                                                                                                                                                                                                                                               /clone="DKFZp7621088"
/clone_lib="762 (synonym: hme
/tissue_type="melanoma (MeWo
/dev_stage="adult"
                                                                                                                                                                                                   /note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
51 c 71 g 192 t
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                   'lab_host="DH10B"
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52.1%;
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                                                                                         CCATAAATATCCATGATAAATCCATTAATCTCATGGATAAAAATTTATATGGTTATACAG 1192
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 ATAACTGGATTTTAATAAAAGTATTTAGTACTTAATACAATTAAAAA
                                                                AACGTAGTATAGTTAATTATTTGTTTACAGGAATGAAAAATTTNCATTAATAATG
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CDNA 5' simil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biomphalaria glabrata
Eukaryota; Metazoa; Mollusca; Gastropoda;
Basommatophora; Planorbidae; Biomphalaria
1 (bases 1 to 243)
1 (bases 1, 243)
1 (bases 1, 243)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR Bloinformatics
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   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  /map='MMU16G3-C4 region; MMU16G3-C4 region"
/clone_lib="B. glabrata adult cerebral ganglia"
/tissue_type="cerebral ganglia"
/note="Organ: brain; Vector: pBLuescript SK-; Site_1:
| Cerebral ganglia | Potal RNA was purified from adult cerebral ganglia exposed to S. mansoni miracidia. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene."

a 12 c 26 g 98 t 3 others
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/strain="BS-90"
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W95009.1
EST.
                                       wysou9 640 bp mRNA
zh46d04.rl Soares_fetal_liver_spleen_
clone IMAGE:415111 5', mRNA sequence.
w95009
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University of Tsukūba, Ibaraki 305, Japan
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu8sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental cDNA in Dictyostelium discoideum (1999)
Unpublished (1999)
On Feb 17, 1998 this sequence version replaced gi:2889714.
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AU076358 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSA642, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Hideko Urushihara
Institute of Biological Sciences
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/strain="AX4"
/db_xref="taxon:44689"
/clone="SSA642"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Dictyostelium discoideum
/dev_stage="slug"
30 c 26 g 157 t 3 ot
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D; Mismatches 169;
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ATTATTAAGCTCTATAACAGCCTTCACTTTGAAAGATTTCAAAGCAGTAAT
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                                                                                                                                                                        TGATGATATCGAATTGCTCAAGAAAATCCTAGCTTATTTTCTACCCGAGGATACCATTCT 839
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                                                                                                   TAAAGGCGGTCATTATGACAACCAACTGCAAAATGGCATCAAGCGAGTAAAAGAGTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL;

This clone is available royalty-free through LLNL;
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/db_xref="GDB:1323581"
/db_xref="taxon:9606"
/clone="IMAGE:415111"
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 TACTGGTCGTGGTTATTCAGTTTTAGAGATGGTGGGAGCATTAAAACAAGCATCACATAA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 TACTGGTCATGGTTCTTCAGTTTTAGAAGAATTGGTTCAGTTAGTCAAAGATAAAAATAT 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189551.
                                                                                                                                                                                                                                                                                                                                           AI808691 506 bp mRNA EST 07-JUL-1999 wf57a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359670 3' similar to TR:015036 O15036 KIAA0322 ;, mRNA
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On Jun 5, 1998 this sequence version replaced (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU061085 685 bp mRNA EST 20-MAY-1999
AU061085 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 506)
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Yoshino, R., Morio, T. and Tanaka, Y.
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T = Dictyostelium discoideum
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/map="869E11; 8; 8q12.3-8q13.3"
/clone="SLC892"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
101 c 94 g 246 t
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/strain="AX4"
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
Basommatophora; Planorbidae; Biomphalaria.
                  The Institute for Genomic Research 9712 Medical Center Drive Booksit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST188689 B. CDNA 5' simi
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq_primer: -40UP from Gibco
                                                                  Bioinformatics
                                                                                  Contact: Kerlavage, AR
                                                                                                                                                    identification of RFLP markers
Malacologia 39 (1-2), 175-182
                                                                                                                                                                                                 Expressed sequence tags (ESTs) of Biomphalaria glabrata, an intermediate snail host of Schistosoma mansoni: Use in the
                                                                                                                                                                                                                                                                   1 (bases 1 to 239)
Knight,M., Miller,A.N., Geoghagen,N.S.M., Lewis,F.A. and
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                                                                                                                                                                                                                                              Kerlavage, A.R.
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Medical Center Drive, 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 B. glabrata adult cerebral ganglia Biomphalaria glabrata
similar to mitochondrial, mRNA sequence.
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATAAATATCCATGATAAATCCATTAATCTCATGGATAAAAATTTATATGGTTATACAG 1192
                                                                                                                                                                                                                                                                                                                                                                                   Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M. Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                   3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan Email: d402hu@sakura.cc.tsukuba.ac.jp PROJECT = 'Dictyostelium discoideum cDNA proj
                                                                                                                                                                                                                  Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                       DNA Res. 5 (6), 335-340 (1998)
99156227
On Jan 17, 1998 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyostelium.
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85; Conserv
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Email: arkerlav
                                                                                                                                                                                                                                                                                                                                                                          development
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                                                                                                                                                                                                                                                                                                       17, 1998 this sequence version replaced gi:1900417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arkerlav@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="B. glabrata adult cerebral ganglia"
/tissue_type="cerebral ganglia"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Total RNA was purified from adult cerebral ganglia exposed to S. mansoni miracidia. CDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene."
a 14 c 25 g 99 t 3 others
/db_xref="taxon:44689"
/map="11; 11, 1.71cR from WI-6355"
/clone="SSA746"
                                                              /organism="Dictyostelium/strain="AX4"
                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Biomphalaria glabrata"
/strain="BS-90"
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Best Local Simi
Matches 109;
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319
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TAGCGAGGCAACTGGAAAATTAAATACTAGCGTTTTTGATAATGAAGATAA 369
              GAGCGAGAAAAAATAGTCTCGATAAAGGACTTTCTTGGAAGTGAGAATAA 1319
                                                     TAATGATATCGATATTGAAGGACAAAATAGAATTTCAACAACCACAATTTCAAAGAATGT 318
                                                                       AGCCAGCGCAGAGTACAAAATTCTCGAGAAAATGCCTCAAACCACCATTCAGGTGGATGG 1268
                                                                                                              TAAATCCATTAATCTCATGGATAAAAATTTATATGGTTATACAGATGAAGAGATTTTTAA 1208
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                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                   266
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                              /clone_lib="Dictyostelium discoideum SS (H:Urushihara)"
/dev_stage="slug"
39 c 41 g 147 t 3 others
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                                                                                                                                                                                                                                          Score 37; DB
Pred. No. 23;
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CCV-C54 spike gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      residua postis v antigen and F1 antigen or their protective protein parts - useful in vaccine for protection against plague C claim 41; Page 65-69; 98pp; English.

A gene fusion (T38249) comprises coding sequences for the Yersinia pestis F1 antigen (see also T38248) including the signal sequence and for the Y. pestis V antigen (see also T38243), joined by a sequence encoding a 6-amino acid peptide linker. It was obtd. by CR amplification of the individual genes using primers (see also T38245) based on the genes and including linker sequences. The gene fusion (see also T38256) can be used to produce F1/V fusion protein (W01044) in transformed cells, esp. gut-colonising corganisms, to induce an immune response against Y. pestis, the causative organism of plague.

Sequence 1530 BP; 499 A; 296 C; 312 G; 423 T;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 1494;
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19-SEP-1996: G00571.

13-MAR-1996: GB-00509.

15-SEP-1995: GB-018946.

05-DEC-1995: GB-024825.

(MINA) UK SEC FOR DEFENCE.

Bennett AM, Leary SEC, Oyston PC
WPI: 96-433824/43.

P-PSDB: W01044.
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Chimeric
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Y. pestis FI/V antigen gene fusion.
Plague; vaccine; genetic immunisati
Fl antigen; cafl; ds.
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                                           TCACTCTTACATATAAGGAAGGCGCTCCAATTACAATTATGGACAATGGAAACATCGATA
                                                                                                                                           ATATGAAAAAATCAGTTCCGTTATCGCCATTGCAATTATTTGGAACTATTGCAACTGCTA 127
CAGAATTACTTGTTGGTACGCTTACTCTTGGCGGCTATAAAACAGGAACCACTAGCACAT
                                                                                                                                                                                                                                           ATATGAAAAAATCAGTTCCGTTATCGCCATTGCATTATTTGGAACTATTGCAACTGCTA
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94; Conservative
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/note= "base T at position 1522 was
from G to create a second in frame
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0; Mismatches
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Result

Score 1472

Query Match

Length

DВ

Description

pestis F1/V

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Database

N\_Geneseq\_36

311585 seqs, 125096042 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Scoring table:

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Title: Perfect score:

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Best Local Sin
Matches 1431;
                                                                                                                                                                                                  rersinia pestis V antigen and F1 antigen or their protective pertopic parts - useful in vaccine for protection against plague bisclosure; page 51-55; 98pp; English.

C A gene fusion (T38256) comprises coding sequences for the versinia pestis F1 antigen (see also T38244) (without the signal sequence) and for the Y. pestis V antigen (see also T38243), joined by a sequence encoding a 6-amino acid peptide linker. It was obtd. by PCR amplification of the individual genes using primers (see also T38245) based on the genes and including linker sequences. The gene fusion (see also T38249) can be used to produce FI/V fusion protein (W01045) in transformed cells, esp. gut-colonising organisms, to induce an immune response against Y. pestis, the causative organism of plague.

Sequence 1462 BP; 476 A; 285 C; 301 G; 400 T;
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19-SEP-1996.

13-MAR-1996; GB-0571.

13-MAR-1995; GB-018946.

15-SEP-1995; GB-018946.

05-DEC-1995; GB-024825.

(MINA) UK SEC FOR DEFENCE.

Bennett AM, Leary SEC, Oys:

WPI; 96-433824/43.
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Plague; vaccine; gene
F1 antigen; caf1; ds.
Chimeric Versinia pes
Chimeric synthetic.
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                                                                                                                                                                                                                                                                Recombinant DNA expressing versinia pestis V antigen - useful in recombinant DNA expressing versinia pestis V antigen - useful in radial or parenteral vaccines for protection against plague set lain 6; Page 11-13; 25pp; English.

Claim 6; Page 11-13; 25pp; English.

Crant of the mature V protein of Versinia pestis. The protein was a fusion protein with maltose binding protein or versinia pertice. The protein or versinia pertice in a different plasmid vectors. Y. pestis is glutathione- S-transferase in 3 different plasmid vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (LcrV) is an unstable 37.3 kba monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/ peptide are useful in vaccines to protect against plague.

Sequence 1014 BP; 346 A; 181 C; 201 G; 286 T;
                                                                                                                          Query Match
Best Local S
Matches 978
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T04222;
18-APR-1996 (first entry)
Partial LcrV (V antigen) gene of Y. p.
LcrV; V antigen; virulence; plague; v.
Yersinia pestis.
Key
Location/Qualifiers
cds
1. 990
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06-MAR-1995;
08-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1994; GB-004577.
(MINA ) UK SEC FOR DEFENCE.
Leary SEC, Titball RW, Williamson WPI; 95-328268/42.
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978; Conser
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Pred. No. 7.2e-251;
0; Mismatches 2;
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T38242;
28-DEC-1996 (first entry)
Y. pestis lcrV (V antigen)
Plague; vaccine; genetic i
F1 antigen; ds.
                                                Key
                            misc_feature
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                                                                   pestis
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PT Yersinia pestis V antigen and F1 antigen or their protective PT epitopic parts - useful in vaccine for protection against plague PS Claim 5; Page 25-28; 98pp; English.

CA lorV gene sequence (T38242) codes for the Yersinia pestis V CC antigen (W01040), which is capable of evoking protective immune CC responses in animals. The gene was amplified from V, pestis CC DNA, by PCR using primers (T38250-51) homologous to the 5' and 3' CC ends of the gene. The gene was inserted into vector pMAL-p2, CC pMAL-c2 or pGEX-5x-2 (see also T38244) to allow prodn. of CC recombinant V antigen for use in vaccines against plague.

CE Expression in gut-colonising organisms and attenuated Salmonella CC typhi allows prodn. of live vaccines. F1/V antigen fusions were calso created (see also T38249 and T38256). The gene can itself be considered to vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.7
Matches 977; Conservative
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19-SEP-1996;
13-MAR-1996; G00571.
13-MAR-1995; GB-005059.
15-SEP-1995; GB-018946.
05-DEC-1995; GB-024825.
 1127
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Bennett AM, Leary SEC, Oyston
WPI; 96-433824/43.
P-PSDB; W01040
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19 SEP-1996.
13-MAR-1996; GB-005059.
13-MAR-1995; GB-005059.
13-MAR-1995; GB-005059.
13-MAR-1995; GB-018946.
15-SEP-1995; GB-018946.
15-DEC-1995; GB-024825.
16-DEC-1995; GB-024825.
17 Bennett AM, Leary SEC, Oyston PCF, Titball RW, Williamson ED WHI, 96-433824/43.
18 WPI; 96-433824/43.
19 P-PSDB; W01041.
19 Yersinia pestis V antigen and F1 antigen or their protective epitopic parts - useful in vaccine for protection against plague of the person sequence (T38243) codes for the Yersinia pestis V antigen (W01041), which is capable of evoking protective immune reponses in animals. The gene was amplified from Y. pestis capable of evoking protective immune reponses in animals. The gene was amplified from Y. pestis of the yer was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis of the yer was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses reponses in animals. The gene was amplified from Y. pestis reponses in animals. The gene was amplified from Y. pestis reponses reponses
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PP PSDB; R79962.

PT Recombinant DNA expressing Yersinia pesus.

PT Recombinant DNA expressing Yersinia pesus.

PT Recombinant DNA expressing Yersinia pesus.

PT oral or parenteral vaccines for protection against plague

PS Claim 6; Page 15-16; 25pp; English.

CC T04222-23 are DNA sequences (lcrV) encoding all or a protective epitopic

CC part of the mature V protein of Yersinia pestis. The protein was

CC expressed as a fusion protein with maltose binding protein or

CC glutathione- S-transferase in 3 different plasmid vectors. Y. pestis

CC is the highly virulent causative organism of plague in a wide range of

CC monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen

CC is postulated to act as a virulence antigen, and transformed

CC minals contg. recombinant DNA encoding a V antigen protein/

neptide are useful in vaccines to protect against plague.

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Yersinia
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Partial LcrV (V antigen) getterv; V antigen; virulence;
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18-APR-1996 (fir
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Leary SEC, Titball RW, Williamson
WPI; 95-328268/42.
P-PSDB; R79962.
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14-SEP-1995.
06-MAR-1995; G00481
08-MAR-1994; GB-004577
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Key
CDS
                                                         Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 8; Page 51; 75pp; English.

This is the nucleotide sequence of a Yersinia pestis Fl antigen, in the method of the invention. Plasmid and host cells are used
                                                                                                                                                                                                   WO9824912-A2.
11-JUN-1998.
04-DEC-1997; U22617.
04-DEC-1996; US-767115.
                                                                                                                                                                                                                                                                                                                                       26-OCT-1998 (first entry)
Nucleotide sequence of F1 ant
F1 antigen; plasmid; vaccine;
                              in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable
                                                                                                                                                                      (HESK-) HESKA CORP.
Haanes EJ, Osorio JE, Thomas
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of F1 antigen nYpF1(a)sec544
from contracting 164 A; 120 C;
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114
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Best Local Similarity
Matches 522; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q92819 standard; DNA; 542 E
Q92819;
17-DEC-1995 (first entry)
Yersinia pestis caf1 (F1);
WO9518231-A1.

06-JUL-1995.
23-DEC-1994; G02818.
24-DEC-1993; GB-026425.

(MINA ) UK SEC FOR DEFENCE.
Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson WPI; 95-246396/32.

P-PSDB; R76528.

DNA constructs capable of transforming microorganisms - whiused as live or attenuated vaccines which induce an immune
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536. .541
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0; Mismatches 8;
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Best Local S
Matches 518
                                                                                           ze-DEC-1996 (first entry)
Y. pestis F1 antigen caf1 gene (including Plague; vaccine; genetic immunisation; F1 V antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against Yersinia pestis, at mucosal surfaces. Disclosure; Page 19-20; 27pp; English. The sequence represents the plasmid pFORFIb including the entire Y. pestis cafl (FI) antigen gene having a 5' tail incliding a SacI restriction site, and up to TATAG downstream of the cafl ORF. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, and are parenterally and orally active vaccines offering protection against bubonic and pneumonic
 WO9628551-A1.
19-SEP-1996.
                                                                                                                                                T38248 standard; DNA; 547 T38248;
                                  mat_peptide
                                                           signal_peptide
                                                                                     Yersinia
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nes 518; Conserv
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                       92. .53
/*tag=
                             /*tag=
.538
                                                                                     strain GB
                                                            29. .91
                                                                      Location/Qualifiers
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Pred. No. 1.
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                                                                                                            signal sequence)
antigen; cafl;
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Matches
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13-MAR-1995; GB-005059.
15-SEP-1995; GB-018946.
05-DEC-1995; GB-024825.
(MINA ) UK SEC FOR DEFENCE.
Bennett AM, Leary SEC, Oys
WPI; 96-433824/43.
P-PSDB; W01043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rersinia pestis V antigen and F1 antigen or their protective epitopic parts - useful in vaccine for protection against plague Claim 41; Page 61-62; 98pp; English.

A DNA sequence (T38248) comprises the cafl gene, including the signal sequence, coding for the F1 antigen (W01043) of Yersinia pestis. It was obtd. by PCR amplification (see also T38257-58) of Y. pestis DNA. The PCR product was cloned into plasmid pBKCMV and the resulting plasmid (pF1AB) was used to transform E. coli No Blue. Purified plasmid, when administered by i.m. injection, induced an immunoglobulin response to F1 in BALB/C mice. Live vaccines comprising gut colonising organisms transformed with the cafl gene (see also T38244) can be used to protect a host animal
                                     V41596;
V41596;
26-OCT-1998 (first entry)
Nucleotide sequence of Fl antigen nYpFlsec510.
Fl antigen; plasmid; vaccine; plague; ds.
Yersinia pestis.
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                                              standard;
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                                               DNA;
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Pred. No. 1.8e
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No. 1.8e-128;
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V41595 standard; DNA; 510 BP.
V41595;
26-OCT-1998 (first entry)
Nucleotide sequence of F1 antig
F1 antigen; plasmid; vaccine; p
Yersinia pestis.
WO9824912-A2.
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Haanes EJ, Osorio JI
WPI; 98-333331/29.
P-PSDB; W59783.
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11-JUN-1998.
04-DEC-1997;
04-DEC-1996;
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This is the nucleotide sequence of a Yersinia pestis F1 antigen, u in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable protecting an animal from contracting plague.

Sequence 544 BP; 166 A; 118 C; 112 G; 148 T;
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                                                                                                                                                                                                                                                                                                                                                        CTCCTAAGGTAAACGGTGAGAACCTTGTGGGGGGATGACGTCGTCTTGGCTACGGGCAGCC
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US-767115.
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/product=
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ine; plague;
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Pred. No. 1.
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1.8e-128;
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04-DEC-1997; U22617.
04-DEC-1996; US-767115.
(HESK-) HESKA CORP.
Haanes EJ, Osorio JE, Thomas RI
WPI; 98-333331/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 8; Page 53; 75pp; English.

This is the nucleotide sequence of a Yersinia pestis Fl antigen, us in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable opituceting an animal from contracting plague.

Sequence 510 BP; 153 A; 114 C; 106 G; 137 T;
                                                                            26-OCT-1998 (first entry)
Nucleotide sequence of F1 antigen nYpF1mat474
F1 antigen; plasmid; vaccine; plague; ds.
W09824912-A2.
11-JUN-1998.
04-DEC-1997; U22617
                                                                       Yersinia
                                                                                                            V41600 standard;
V41600;
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Best Local Similarity
Matches 454; Conser
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(HESK-) HESKA CORP.
Haanes EJ, Osorio JI
WPI; 98-333331/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 8; Pages 59-60; 75pp; English.

This is the nucleotide sequence of a Yersinia pestis F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.

Sequence 474 BP; 143 A; 106 C; 99 G; 126 T;
                                                                                                                                                            17-pgc-1995 (first entry)
Yersinia pestis cafl (F1) antigen in plass
Vaccine; antigen; Salmonella typhimurium;
bubonic plague; pneumonic plague; ds.
                                                                                                                                                                                                      Q92817 standard;
Q92817;
17-DEC-1995 (fi
W09518231-A1.
06-JUL-1995.
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                                                                                             misc_feature
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                                                   /*tag= b
/note= "lacz
536. .541
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1. .6
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Pred. No. 1.9e-111;
0; Mismatches 2;
                                                                 promoter
                          pFGAL2a
                                                                                                                                                                           in plasmid pFGAL2a.
imurium; Salmonella typhi;
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AC T3
DT 28
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KW V
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The sequence represents the plasmid pFGAL2a construct showing the fusion of the first few bases of beta-galactosidase in the vector with the Y. pestis cafl (F1) antigen minus its signal sequence and having a 5' tail including a SacI restriction site, and up to the cafl AACC-3' end with some vector bases. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, and against bubonic and pneumonic plague.
Sequence 541 BP; 163 A; 120 C; 111 G; 147 T;
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Best Local Similarity
Matches 454; Conserv
                                                           T38244 standard;
T38244;
Z8-DEC-1996 (fi
Y. pestis cafi
                                    Plague; vaccine;
V antigen; ds.
             Key
                          Yersinia
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24-DEC-1993; GB-026425
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                                                                                                      standard;
                         pestis
                                               (first entry)
if1 (F1 antigen) gene.
ine; genetic immunisation;
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Location/Qualifiers
1. .6
                          strain
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Pred. No. 2.8e-111;
0; Mismatches 3;
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Best Local Similarity
Matches 454; Conser
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19-SEP-1996.
13-MAR-1996; GB-00571.
13-MAR-1995; GB-018946.
15-SEP-1995; GB-024825.
(MINA) UK SEC FOR DEFENCE.
Bennett AM, Leary SEC, Oyston PC
WPI; 96-433824/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis V antigen and F1 antigen or their protective epitopic parts - useful in vaccine for protection against plague claim 7; Page 43-45; 98pp; English.

The caf1 gene (T38244) codes for the Yersinia pestis F1 antigen (W01042), which is capable of evoking protective immune responses in animals. The gene was amplified from Y. pestis DNA by PCR using primers (T38245-46) homologous to the 5' and 3' ends of the gene. The caf1 PCR product was ligated into pUC18 and transformed into E. coli JM109 to produce vector pFGAL2a. The caf1 gene can be used to produce recombinant F1 antigen for use in vaccines against plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression in gut-colonising organisms and attenuated Salmonelia typhi allows prodn. of live vaccines. The gene can itself be used in genetic vaccines. F1/V antigen fusions were also created (see also T38249 and T38256).

Sequence 541 BP; 163 A; 120 C; 111 G; 147 T;
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ATGCTGTAACCGTAACCGTATCTAACCAAGAATTCAT
                                                                                                                           CTAAGGTAAACGGTGAGAACCTTGTGGGGGGATGACGTCGTCTTGGCTACGGGCAGCCAGG
                                                                                                                                                                               ATAACCACCAATTCACTACAAAAGTGATTGGCAAGGATTCTAGAGATTTTGATATCTCTC
                                                                                                                                                                                                                                                                                                AATTACTTGTTGGTACGCTTACTCTTGGCGGCTATAAAACAGGAACCACTAGCACATCTG
                                                                                                                                                                                                                                                                                                                                                      CTCTTACATATAAGGAAGGCGCTCCAATTACAATTATGGACAATGGAAACATCGATACAG
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                                                                                  ATTTCTTTGTTCGCTCAATTGGTTCCAAAGGCGGTAAACTTGCAGCAGGTAAATACACTG
                                                                                                              CTAAGGTAAACGGTGAGAACCTTGTGGGGGATGACGTCGTCTTGGCTACGGGCAGCCAGG
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/note= "includes the first few bases of
beta-galactosidase sequence in vector
pFGALZa"
2. .457
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Pred. No. 2.8e
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.8e-111;
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Disclosure; Page 17-18; 27pp; English.

The sequence represents the plasmid pFSIG3a construct showing the fusion of the first few bases of the E. coli LTB signal sequence with the Y. pestis cafl (FI) antigen minus its signal sequence and having a 5' tail including a SacI restriction site, and up to the cafl AACC-3' end with some vector bases. The DNA construct can be specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, and against bubonic and pneumonic plague.

Sequence 542 BP; 163 A; 122 C; 110 G; 147 T;
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    Matches 454; Conservative
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Q92818;
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Yersinia pestis caf1 (F1) antigen in plasmid pFSIG3a.
Yaccine; antigen; Salmonella typhimurium; Salmonella typhi;
bubonic plague; pneumonic plague; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA constructs capable of transforming microorganisms - which can be used as live or attenuated vaccines which induce an immune response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1995.
23-DEC-1994; G02818.
24-DEC-1993; GB-026425.
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MINA ) UK SEC FOR DEFENCE.
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                                                                                                                                                                                                                                                                                        125
    305
                                                                                                                   185
                                                                                                                                                                                                                                                               681
                                                                                                                                                                                                                                    65
TCCTAAGGTAAACGGTGAGAACCTTGTGGGGGATGACGTCGTCTTGGCTACGGGCAGCCA 488
                                                                                                                                                                                                                                                 CACTCTTACATATAAGGAAGGCGCTCCAATTACAATTATGGACAATGGAAACATCGATAC 248
                                                                                                                                                                                        AGAATTACTTGTTGGTACGCTTACTCTTGGCGGCTATAAAACAGGAACCACTAGCACATC 308
                                                       AAATAACCACCAATTCACTACAAAAGTGATTGGCAAGGATTCTAGAGATTTTGATATCTC 428
                                                                                                                TGTTAACTTTACAGATGCCGCGGGTGATCCCCATGTACTTAACATTTACTTCTCAGGATGG
                                                                                                                                 TGTTAACTTTACAGATGCCGCGGGTGATCCCATGTACTTAACATTTACTTCTCAGGATGG 368
                                                                                                                                                                         AGAATTACTTGTTGGTACGCTTACTCTTGGCGGCTATAAAACAGGAACCACTAGCACATC 184
                                                                                                                                                                                                                                  CACTATTACATATAAGGAAGGCGCTCCAATTACAATTATGGACAATGGAAACATCGATAC
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/note= "E. coli LTB signal peptide bases"
536. .541
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1. .6
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/note= "vector
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98.9%;
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                                                                                                                                                                                                                                                                                                                                                 Score 451; DB 1;
Pred. No. 5.9e-111;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Titball RW,
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                                                                                                                                                                                                                                                                                                                                                                            Length 542;
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Search completed: November 27, 1999, 19:34:03 Job time: 2661 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM of: US-08-699-716A-2 to: Issued_Patents_NA:*
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Database length: 52875861
Search time (sec): 50.310000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZSCORE ESCORE Len (2912_6/ptodata/1/ina/5B_COMB.seq:US-08-480-604A-25 (2912_6/ptodata/1/ina/5D_COMB.seq:US-08-495-496A-25 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-332-766A-1 5 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-322-766A-1 5 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-22-766A-1 5 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-22-766A-1 5 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-22-766A-1 5 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-22-766A-1 5 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-22-766A-1 5 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-22-766A-1 (2912_6/ptodata/1/ina/5C_COMB.seq:US-08-22-76-76-76-76-76-76-76-76-76-76-76-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -Q=/cgn2_1/USPTO_spool/US08699716/runat_27111999_151715_6599/app_query.fasta
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=11.000
-GAPEXT=11.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NCPU=6 -ICPU=3 -WAIT -DM_MEM=28000 -PM_MEM=15000 -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -OGAPOP=4.500 -QGAPEXT=0.050 -START=1 -DTRANS -MATRIX=pam150
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=escore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MODEL=sw.model -DEV=xlp
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2_6/ptodata/1/ina/5D_COMB.seq:US-08-255-457-2 1+ 60.00
2_6/ptodata/1/ina/5C_COMB.seq:US-08-255-457-2 1+ 60.00
2_6/ptodata/1/ina/5C_COMB.seq:US-08-332-766A-28 4- 56.00
2_6/ptodata/1/ina/5C_COMB.seq:US-08-961-539-3 1+ 58.00
2_6/ptodata/1/ina/5C_COMB.seq:US-08-961-539-3 1+ 60.00
2_6/ptodata/1/ina/5A_COMB.seq:US-08-160-670A-3 1+ 49.0
2_6/ptodata/1/ina/5A_COMB.seq:US-08-155-171B-27 3+ 49.0
2_6/ptodata/1/ina/5A_COMB.seq:US-08-155-171B-27 3+ 49.0
2_6/ptodata/1/ina/5A_COMB.seq:US-08-155-171B-27 3+ 49.0
2_6/ptodata/1/ina/5A_COMB.seq:US-08-155-171B-27 3+ 49.0
2_6/ptodata/1/ina/5A_COMB.seq:US-08-155-171B-28 5- 49.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ptodata/1/ina/5B_COMB.seq:US-08-068-747-8 5-
/ptodata/1/ina/5B_COMB.seq:US-08-563-864-1 2+
/ptodata/1/ina/PCTUS9_COMB.seq:ECT-USS5-06839-1
                                                                                                                                                                                                                                /ptodata/1/ina/PCTUS9_COMB.seq:PCT-US95-09383-1
/ptodata/1/ina/5A_COMB.seq:US-07-882-292-1 2+
/ptodata/1/ina/PCTUS9_COMB.seq:PCT-US93-04102-1
                                                                                                                                                                                                                                                                                                                                            /ptodata/1/ina/5D_COMB.seq:US-08-435-998-28;
/ptodata/1/ina/5B_COMB_seq:US-08-759-848-1 5-
                                                                                                                            /ptodata/1/ina/5B_COMB
                                                                                                                                                        ptodata/1/ina/5D_COMB.seq:US-08-690-011A-12
ptodata/1/ina/5A_COMB.seq:US-08-333-358-11 1
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-2 1+ 60.00 139.62 3.33

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55784 - 56.00 137.85 4.18

-3 1+ 58.00 137.57 4.33

-1 1+ 60.00 137.43 4.41
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                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-480-604A-25
                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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Quality:
Ratio:
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seq_documentation_block:
                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION: NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-480-604A-25
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                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALIFORNIA
UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                               (415)
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PADHYE, NISHA V.
                                                                                                                                             linear
E: DNA (genomic)
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                                                                                                                                                                                                                                                                                             (415) 705-8410
415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLEN & CARROLL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ication US/08480604A
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93.00
5.167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 08/329,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/429,791
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T, SUITE 2200
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alignment_block: US-08-699-716A-2 \times US-08-480-604A-25 (1)
                                                                                                               ; NAME/KEY: CDS; LOCATION: 1...
US-08-405-496A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Patent No. 5919665
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, J
TITLE OF INVENTION: VA
; TITLE OF INVENTION: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-405-496A-25
Quality: 93.00
Ratio: 5.167
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q_documentation_block:
Sequence 25, Application US/08405496A
Patent No. 5919665
                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                     TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/985,321 FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 220 MONTGOMERY STREET, CITY: SAN FRANCISCO
                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                    H: 1402 base pairs nucleic acid IDEDNESS: double
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 Length: 18
Gaps: 0
Percent Identity: 94.444
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                                                                                                                                                                                                                                                                                                                                                                           OPHD-01308
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alignment_block: US-08-699-716A-2 x US-08-405-496A-25
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seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-600-783-15
                                                                                                                                                             alignment_block:
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                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 861-3000
TELEPHAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 base pairs
TYPE: nucleic acid
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                                                                                                                                          US-08-699-716A-2 x US-08-332-766A-1/rev (5)
                                                                                                                                                                                                 Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: BIRD, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-NOV-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE T
NUMBER OF SEQUENCES: 125
                                   37 ННННННННННСҮОЕЕЕОЕК 18
                                                                     3 HHHHHHHHHHSSGHIDDDDK
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 New CITY: Washington STATE: D. C.
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                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RY: U.S.A.
20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08332766A
                                                                                                         to reverse of: US-08-332-766A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1994
                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                 4.059
85.000
                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                    69.00
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                                                                     22
                                                                                                                                                                                                 Gaps:
Percent Identity:
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                                                                                                                                                                                                                                    Length:
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                                                                                                                                                                                                 55.000
                                                                                                         from: 1
                                                                                                         ţo:
                                                                                                          377
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Sequence 15,

Application US/08600783

tent No.

\_documentation\_block:

GENERAL INFORMATION:

APPLICANT:

SHIN, Hang Cheol CHANG, Seung Gu

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alignment_scores:
                                                                              ; ANTI-SENSE: US-08-600-783-15
                                                                                                                                                                        TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 bases
                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KIM, Dae Young
APPLICANT: KIM, Chong Suhi
TITLE OF INVENTION: Proinsulin Derivative and Process
TITLE OF INVENTION: for Producing Human Insulin
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-2751
FILING DATE: 15-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk,
COMPUTER: IBM PC/AT
                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Taegu
STATE: Taegu
                                                                                                                             TOPOLOGY:
                                                                                                                                         STRANDEDNESS:
                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Rep
ZIP: 706-040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: KIM, Chong Suhl
STREET: Garden Heights Apt. 202-801,
STREET: Hwangkeum-dong, Soosung-ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Bucheon-shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: KIM, Dae Young
STREET: Sosa Jukong Apt. 108-202, Sosa Bon-dong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Kwangmyung-shi
STATE: Kyungki-do
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 Quality:
Ratio:
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Ssangma-Hanshin Apt.
#245 Cholsan-dong
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                                                                                              no
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undai Apt. 71-203, Apkujong-dong,
                                                                                                           primer DNA
 62.00
5.636
                                                                                                                                       single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5 inch, 1.44MB storage
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Length:
Gaps:
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alignment_block: us-08-699-716A-2 \times us-08-600-783-15 (1)
                                                                                                     alignment_block:
US-08-699-716A-2 x US-08-068-747-8/rev (5)
                                                                                                                                                                                                                                                                      ; MOLECULE TYPE:
; DESCRIPTION:
US-08-068-747-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-068-747-8
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                                                                                                                                                      Quality: 60.00
Ratio: 6.000
Percent Similarity: 100.000
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                                                                   Align seg 1/1 to reverse of: US-08-068-747-8 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08068747 Patent No. 5695933
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hudson, TAPPLICANT: Housman, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granaban, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/068,747 FILING DATE: 28-MAY-1993
                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                    ннининини 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Hamilton, Brook,
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schalling, Martin
Hudson, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         617-861-6240
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                                                                                                                                                                                                                                                                                                        other nucleic acid
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                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                         "Synthetic"
                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 100.000
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                                                                   to:
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seq\_name: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:US-08-563-864-1

New York

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seq_documentation_block:
                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/PCTUS9_COMB.seq:PCT-US95-06839-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-563-864-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 60.00
Ratio: 6.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                              US-08-699-716A-2 x US-08-563-864-1 (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              Sequence 1, Application PC/TUS9506839 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5674687
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CITY: 1
                                                                      APPLICANT: Hershfield, Bennett
TITLE OF INVENTION: A METHOD FOR THE IDENTIFICATION
TITLE OF INVENTION: OF NUCLEIC ACID SAMPLES FROM DNA
NUMBER OF SEQUENCES: 1
                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,395
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: A METHOD FOR THE IDENTIFICATION OF
TITLE OF INVENTION: NUCLEIC ACID SAMPLES FROM DNA-CONTAINING ORGANISMS
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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CITY: Rochester
STATE: New York
                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Goldman Esq., Michael L. REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Clinton Square, P.O. Rochester
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                                      Nixon, Hargrave, Devans & Doyle
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Gaps: 0
Percent Identity: 100.000
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                                                                                                  FROM DNA-CONTAINING ORGANISMS
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alignment_block:
US-08-699-716A-2 x PCT-US95-06839-1 (2)
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FILING DATE: 31-MAI-L.

ATTORNEY/AGENT INFORMATION:

NAME: Goldman Esq., Michael L.

REGISTRATION NUMBER: 30,727

REGISTRATION NUMBER: 19603/160 (D-1452)

REFERENCE/DOCKET NUMBER: 19603/160 (D-1452)

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: PCT-US95-06839-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 60.00
Ratio: 6.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/07781034 Patent No. 5442050
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Fishman,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: UNKNOWN MOLECULE TYPE: DNA MOLECULE TYPE: NO
                                                                                              ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                               CITY: Lexington
STATE: Massachusetts
APPLICATION NUMBER: U
                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                         ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                         Two Militia Drive
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                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                 Molecular Cloning of Antigens Shared By Rat- and Human-Derived Pneumocystis Carinii
                                                                                                                                                                                                                                                                                                                                     Jay A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.25
                 US/07/781,034
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Percent Identity: 100.000
                                                    Version
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ATTORNEY/AGENT INFORMATION:

Granahan, Patricia

CLASSIFICATION:

REFERENCE/DOCKET NUMBER: 32,

MGH91-02A

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alignment_block:
US-08-699-716A-2 x US-07-781-034-4/rev (4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9208328
GENERAL INFORMATION:
APPLICANT: Fishman, Jay A.
TITLE OF INVENTION: Molecular Clor
TITLE OF INVENTION: Rat- and Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MADER: PCT/US92/08328
FILING DATE: 19920930
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,166
FILING DATE: 30-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
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LENGTH: 1189 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 861-6240
             TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 ннининининня 189
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STRANDEDNESS: QUU
STRANDENCY: linear
                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MGH91-02AA PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                       APPLICATION NUMBER: US 0' FILING DATE: 18-OCT-1991
                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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(617) 861-9540
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5.385
86.667
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Molecular Cloning of Antigens Shared By
Rat- and Human-Derived Pneumocystis Carinii
                                                                                                                                                                                                           US 07/781,034
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Gaps: 0
Percent Identity: 80.000
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alignment_block:
US-08-699-716A-2 x PCT-US92-08328-4/rev (4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-332-766A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                  TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1,
Patent No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                             NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Relicurrent application Data: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 НИННИННИННЫЯ 189
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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APPLICANT: ARMOUR, John
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                 STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08332766A 5843647
                                                 : 377 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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DNA (genomic)
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5.385
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                                                                                                                                                                                                                                                                                                                                                                     US/08/332,766A
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alignment_block:
US-08;-699-716A-2 x US-08-332-766A-30/rev (6)
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US-08-699-716A-2 x US-08-332-766A-1/rev (6)
                                                                                                                      alignment_scores:
                                                                                                                                                                                 US-08-332-766A-30
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                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 30, Application US/08332766A Patent No. 5843647 GENERAL INFORMATION:
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Sequence 30, Applicati
                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIF: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 276 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   MOLECULE TYPE:
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APPLICANT: ARMOUR, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: SIMPLE TANDEM REPEATS
UMBER OF SEQUENCES: 125
                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/332,766A FILING DATE: 01-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                    Quality:
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20005-3918
                                                                                                                                                                                                                                                      nucleic acid
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С
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                                                                                                                                                                                               DNA (genomic)
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1.833
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4.571
77.778
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Percent Identity:
                                                             Percent Identity:
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seq_documentation_block:
    Sequence 3, Application PC/TUS9505772
    GENERAL INFORMATION:
                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/PCTUS9_COMB.seq:PCT-US95-05772-3
                                                                                                                                                                                                                                                  alignment_block: US-08-255-457-3 (1)
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                                                                                                                                                                                                                 Align seg 1/1 to: US-08-255-457-3
                                                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Gilbert-Rothstein, Joanne
APPLICANT: Wright, Andrew
TITLE OF INVENTION: HELICOBACTER PYLC
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
                                                                                                                                             10 СИННИННИТИННИУНССЕНИНН 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 ННКННННННННННЫМ 20
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TYPE: n
                                                                                                                                                               2 GHHHHHHHHHHSSGHIDDDDKH 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Clark, Paul C. REGISTRATION NUMBER: 30,162
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                                                                                                                                                                                                                                                                                                                                        Quality:
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02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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Plaut, Andrew G.
Gilbert-Rothstein, Joanne V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 542-8906
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3.750
72.727
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                                                                                                                                                                                                                                                                                                     Percent Identity:
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

Fish & Richardson

TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

APPLICANT: Wright, Andrew TITLE OF INVENTION: HELICOBACTER PYLORI NICKEL

BINDING PROTEIN

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alignment_block:
US-08-699-716A-2 x PCT-US95-05772-3 (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: PCT-US95-05772-3
                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-203-532F-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
TELEPEAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
COUNTRAL
ZIP: 44114-2bbb
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TYPHTER: THE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08203532F Patent No. 5856121
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 183 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                       APPLICANT: Gorski, David H. APPLICANT: Walsh, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 СИННИНИННИННИН 31
                                                                                                                                       STREET: 800 Super CITY: Cleveland STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GHHHHHHHHHHSSGHIDDDDKH 23
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Ratio:
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3.750
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Percent Identity: 54.545
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alignment_block:
US-08-699-716A-2 x US-08-203-532F-3 (3)
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; LOCATION:
US-08-203-532F-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/PCTUS9_COMB.seq:PCT-US95-01882A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9501882A GENERAL INFORMATION:
             FILING DATE:
CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: GOLTICK, Mary E.
REGISTRATION NUMBER: 34829
REFERENCE/DOCKET NUMBER: 2231
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01882A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 941 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter, and Griswold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Growth Arrest Homeobox Gene NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gorski, David H. APPLICANT: Walsh, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                        STREET: 800 Supe
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 СНИННИННИН 87
                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 44114-2688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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(216) 622-8200
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                                   22311/00114
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Perfect score:
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     /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/FDTUS9_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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11406
1100
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US-08-480-604A-25
US-08-23-2463-1
US-08-23-2463-1
US-08-308-872B-5
PCT-US91-08525-31
PCT-US91-08525-31
PCT-US91-08525-31
US-08-785-428-1
US-08-785-428-1
US-08-785-176-5
US-08-206-176-5
US-08-323-1708-1
US-08-323-1708-1
US-08-323-1758-1
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US-08-323-10
US-07-960-932-1
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US-08-137-126-7
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US-08-455-970A-13
US-08-455-970A-13
US-08-387-156-7
US-08-387-156-7
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US-08-694-865-7
US-08-694-865-7
US-08-694-865-7
US-08-694-865-7
US-08-589-711-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Search time 27.29 Seconds (without alignments) 6068.421 Million cell updates/sec
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                 Sequence
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   Sequence
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25, Appl
14, Appl
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36, Appl
17, Appl
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ALIGNMENTS	US-07-741-940-1 US-08-484-105-5 US-08-484-106-5 US-08-289-548A-1 US-08-289-548A-1 US-08-370-335A-1 PCT-US95-07748A-1
	Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

## RESULT 1 US-08-480-604A-25 ; Sequence 25, Application

	TOPOLOGY: linear	
	LENGTH: 1402 b	
	TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:	
	ICATION INFORMATION: E: (415) 705-8410	
	TRATION NUMBER: ENCE/DOCKET NUMBE	
	ATTORNEY/AGENT INFORMATION: NAME: INGOLIA, DIANE E.	
	31-OCT-1989	
	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/429.791	
	FILING DATE: 04-DEC-1992	
	TION DATA:	
	APPLICATION NUMBER: US 08/161,907	
	FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:	
	APPLICATION NU	
	FILING DATE: 10 MAK-1995 PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US 08/422,711	
	PRIOR APPLICATION DATA:	
	FILING DATE: 07-JUN-1995	
	APPLICATION NUMBER: US/	
	CURRENT APPLICATION DATA:	
	SYSTEM: PC-DOS/MS-DOS	
	COMPUTER: IBM PC compatible	
	ER READABLE FORM:	
	COUNTRI: UNITED STATES OF AMERICA ZIP: 94104	
	IFORNIA	
	SAN FRANCISCO	
	CARROLL, LLP	
	NUMBER OF SEQUENCES: 32  CORRESPONDENCE ADDRESS:	
AND	OF INVENTION: F	
	CANT: STAFFORD, DOUGLAS C.	
	APPLICANT: PADHYE, NISHA V. APPLICANT: FIRCA, JOSEPH R.	
	THALLEY, BRUCE	
	GENERAL INFORMATION:  APPLICANT: KINK, JOHN A.	
	o. 5736139	
	) 4 7.	

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US-08-405-496A-25
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                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0CT-1989
                                         MOLECULE TYPE: FEATURE:
                                                                                                                                                                                  REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPTELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/329,154
FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VA
TITLE OF INVENTION: NE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                            FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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LOCATION:
                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/985,321 FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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              LOCATION:
                           NAME/KEY:
                                                                           TOPOLOGY:
                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                        nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                 INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALIFORNIA
                                                                                                                   1402 base pairs
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                            CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                           linear
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                                                        DNA (genomic)
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 Mismatches

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                                                                                                                                                             Query Match 3.1
Best Local Similarity 7.6%
Matches 33; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
REFERENCE/DOCKET NUMBER: 3
                                                                                              1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
1093 ATTCAAGCCGAAATTAATAAGCATCTGTCTAGTAGTGGCACCATAAATATCCATGATAAA 1152
                                 1416
                                                             1033 CGTAGCAAGTTGCGTGAAGAATTAGCTGAGCTTACCGCCGAATTAAAGATTTATTCAGTT 1092
                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                            973 CGTATCGATGATGATATTTTGAAAGTGATTGTTGATTCAATGAATCATCATGGTGATGCC 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Alexandria
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SCHEIFLINGER,
FALKNER, F. G.
                                                                                                                                                                                                                                                          pTZgpt-F1s
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                                                                                                                                                                                                                                                                                                                                                                                                       (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBER: EP 91 114 300.6
26-AUG-1991
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98.2%;
                                                                                                                                                          3.1%; Score 48; DB
7.6%; Pred. No. 0.000
tive 212; Mismatches
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                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                         Length 7218;
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US-08-308-872B-5
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                                                                                                                                                                       TELEPHONE: (301) 258-5
                                                                                                                                                                                                                                                                                              FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 9
FILING DATE: 25-API-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BROWN, Thomas David Kay
APPLICANT: HORSBURGH, Brian Colin
TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1116
                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4435 base pairs
                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,409 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Gormley, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/042,846 FILING DATE: 05-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19-SEP-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
                    ORGANISM:
                                                                                            STRANDEDNESS:
                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20850
                                                                                                                                                                                                                                                       Gormley, Mary E.
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CCV-V54
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                Canine corona virus
                                                                           linear
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                                                                                              single
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; LOCATION: 60..4418
; OTHER INFORMATION:
US-08-308-872B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US91-08525-31
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                                                                                                                         TELEFAX: (215) 270-509
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING 'SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Smithkli
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                    FILING DATE: 13-MAY-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/698,927
FILING DATE: 13-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
FEATURE:
NAME/KEY: CDS
                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                     FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: SB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AATAATGATTGTGTACAAGTTAATGTGACACAATTGCCTGGCAATGAAAATATCATTAAA 179
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19
CLASSIFICATION:
                                                         TOPOLOGY:
                                                                    TYPE: NUCLEIC
STRANDEDNESS:
                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19406-2799
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                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: King of Prussia
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                                                                                                              LENGTH:
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                                                                                         NUCLEIC ACID
                                                                                                                                                                                                                                                    King, William T
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                                                                                                            4365 base pairs
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                                                         unknown
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                                                                        double
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48.8%;
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                                                                                                                                                                                                                    SBC 14532B
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Pred. No. 0.094
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; LOCATION: PCT-US91-08525-31
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Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application PC/TUS9304384 GENERAL INFORMATION:
APPLICANT: Miller, Timothy J.
                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 08-MAY.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 13-MAY-1991
                                                                                    NAME: Schreck, Patrica A.
REGISTRATION NUMBER: 3,77
REFERENCE/POCKET NUMBER: SB
TELECOMMUNICATION INFORMATION:
TELECHONE: (215) 270-5015
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods TITLE OF INVENTION: Against Coronaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Klepfer, APPLICANT: Reed, All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline E
ADDRESSEE: Patents
STREET: 709 Swedeland I
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         746 AAGATTCGGAAGTTTTTGCCAATAGAGTAATTACTGATGATATCGAATTGCTCAAGAAAA 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        686 AATTGGTTCAGTTAGTCAAAGATAAAAATATAGATATTCCATTAAATATGATCCCAGAA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 TACATGCCTTTTATTTTGATATGGAAGCTATGGAAAATAGCACTGGTAATG 298
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER FILING DATE: 1993
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 ATGATTGTAGACAAGTTAACGTAACACAATTAGCTGGCAATGAAAACCTTATTAGAGACT 127
                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTAGCTTATTTTCTACCCGAGGATACCATTCTTAAAGGCGGTCATTATG 856
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   4365 base pairs
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Jones, Elaine V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                         (215)
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19930507
                                                                       270-5090
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                                                                                                          33,777
"PPR: SBC H85009-1
                                                                                                                                                                                                                                                                     US 07/698,927
                                                                                                                                                                                                                                                                                                                        US 07/882,171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.4; DB Pred. No. 0.27;
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    Corporate

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5962267
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.4%;
Best Local Similarity 47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: unk
MOLECULE TYPE:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Proinsulin Derivative and P. TITLE OF INVENTION: for Producing Human Insulin NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
                                                                                                     ADDRESSEE: KIM, Chong Suhl
STREET: Garden Heights Apt. 202-801,
STREET: Hwangkeum-dong, Soosung-ku
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SHIN, Hang Cheol
STREET: Ssangma-Hanshin Apt.
STREET: #245 Cholsan-dong
                                  COUNTRY: Republic of Korea ZIP: 706-040
                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 ATGATTGTAGACAAGTTAACGTAACACAATTAGCTGGCAATGAAAACCTTATTAGAGACT 127
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                                                                    STATE: Taegu
                                                                                        CITY:
                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                ZIP:
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                                                                                      Taegu
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Kyungki-do
                                                                                                                                                                                                               Bucheon-shi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIN, Hang Cheol
CHANG, Seung Gu
KIM, Dae Young
KIM, Chong Suhl
                                                                                                                                                                                                                              E: KIM, Dae Young
Sosa Jukong Apt. 108-202, Sosa Bon-dong,
Sosa-ku
                                                                                                                                                                                                                                                                                                                                                        Kangnam-ku
                                                                                                                                                                                                                                                                                                                                                                        E: CHANG, Seung Gu
Hyundai Apt. 71-203, Apkujong-dong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                      Republic of Korea
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Floppy Disk, 3.5 inch, 1.44MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
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COMPUTER: IBM PC, OPERATING SYSTEM: SOFTWARE: WORD P.

MS-DOS

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Best Local (
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9601096.2

FILING DATE: 19-AN-1996

APPLICATION NUMBER: 9622617.0

FILING DATE: 30-CCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Gimmi, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P31354

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 278-1000
TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5750387el trna Synthetase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-2751
FILING DATE: 15-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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LENGTH: 47 bases
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REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                APPLICATION NUMBER: US/08/785,428 FILING DATE: 17-JAN-1997
                                                                                                                                                                                   CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                              19406-0939
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linear
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                        P31354-5
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                                                                                     TOPOLOGY: US-08-560-007B-4
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   Query Match
Best Local Sin
Matches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08560007B Patent No. 5914248
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Best Local Similarity
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                                                                                                                                                                                      CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2415 base pair
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KUIPERS, OSCAR PAUL APPLICANT: DE VOS, WILLEM MEINDERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 GGTTTAGCATACGTTGATGAAGTTGCAGTTAACTGGTGTCCAGCATTAGGCACTGTTTTA 495
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                                                                                                               LENGTH: 1446
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: dou
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 610-270-5090 TELEX:
                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 17 NOV 1995
                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 700 KOPP
CITY: PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: THE WEBB LAW FIRM STREET: 700 KOPPERS BUILDING,
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                   Similarity
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   Conservative
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                                                                                                      UNKNOWN
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                 2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHOD FOR CONTROLLING THE GENE EXPRESSION IN LACTIC ACID BACTERIA
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                 Score 34.8; DB Pred. No. 0.87;
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Pred. No. 1.1;
Mismatches
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                                 Length 1446;
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; LOCATION:
US-08-179-557-20
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                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 01-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
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APPLICATION NUMBER: 1
FILING DATE: 30-DEC-
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MEDIUM TYPE: Floppy disk
                                                FEATURE:
                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                TELLEFAX: 2004136
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CTTY: Washington,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                               TOPOLOGY:
                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 25-MAI
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 03-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 07-JAN-1994
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                                                                                                              LENGTH:
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o. 5837509
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NILSSON, Dan
VRANG, Astrid
                                                                                                           1100 base pairs
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                                                               linear
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Yersinia enterocolitica
US-09-036-582-36
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APPLICANT: van der Bruggen, Pierre
APPLICANT: Cornelis, Guy R.
TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
TITLE OF INVENTION: WITH RECOMBINANT YERSINIA
FILE REFERENCE: 11154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Appl. Patent No. 596538:
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                                                                                                                                                                                          1190
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                                   1310 GTGAGAATAAAAGA 1323
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                                                                                                             1250 CCACCATTCAGGTGGATGGGAGCGAGAAAAAAATAGTCTCGATAAAGGACTTTCTTGGAA 1309
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                                                                                                                                                                                                                                                                                                      599 gtatattaagtgatagtgaaaatcctttaccccacaataagttggatccgtatctcccgg 658
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                                                                     acaataaatccattatagatggaaaggaattatcagtttcggtacataaaaagagaatag 838
                                                                                                                                                 cgcagggagttggtactgttgttaacaaaaaaaatgaaaccatctttaataggtttgata 778
                                                                                                                                                                                                                            taactttttacaaacatactcaaggtaaaaaacgtcttaatgaatatttaaatactaacc 718
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Pred. No. 1
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RESULT 13
US-08-323-170B-1
Sequence 1, Application US/08323170B;
Patent No. 5733772;
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US-08-206-176-5
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APPLICANT: Garner, Ian
APPLICANT: Dalrymple, Michael
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production
TITLE OF INVENTION: Animals
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 206-548-2329 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE: cLone: human fibrinogen gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 10564 base pai
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           4116 CTTAGCAGTTTCCAAAGAAAATATAAAATT 4145
                                                                                                                                                                                                 4056 TAATTTTACATTTTCCTCAAGAATGGAATAATTTATCAGAAAGCACTTCTTAAGAAAATA 4115
                                                                                                                                                                                                                                                                        3996 TTTGATTTGTTTTTCTTTTTCAAAAAGTTTATAATTTTAATTCATGTTAATTTAGTAATA 4055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                            808 CTAGCTTATTTTCTACCCGAGGATACCATT 837
                                                                                                                                                                                                                                                                                                             688 TTGGTTCAGTTAGTCAAAGATAAAAATATAGATATTTCCATTAAATATGATCCCAGAAAA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Parker, Gary E REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                     GATTCGGAGGTTTTTGCCAATAGAGTAATTACTGATGATATCGAATTGCTCAAGAAAATC 807
                                                                                                                                                                                                                                                                                                                                                     l Similarity
77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: ZymoGenetics, Inc.
4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dalrymple, Michael
Prunkard, Donna E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                   2.1%;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                   Sequence 13, Application US/08229145
Patent No. 5691461
GENERAL INFORMATION:
APPLICANT: Hoke, Glenn D.
APPLICANT: Ecker, David J.
TITLE OF INVENTION: INHIBITION OF CANDIDA USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor.
                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                   7199 AACTTCTCATGTAATTGTTATAATCCAGAAAAACATGTATATGGTACTATGCAAGTTGAG 7258
                                                                                                                                                                                                                                                                                                                                                                                                      7139 TITAAAAATCATTATTCTACAGCATATGCTAAAGTACCAGATACCTTTAATTCTATTATT 7198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen,
                      CORRESPONDENCE
                                                                                                                                                                                                                                                              7259 TCTGATAATCGAAATTTTGATA 7280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                              403 AAGGATTCTAGAGATTTTGATA 424
                                                                                                                                                                                                                                                                                                                                                                     343 TACTTAACATTTACTTCTCAGGATGGAAATAACCACCAATTCACTACAAAAGTGATTGGC 402
                                                                                                                                                                                                                                                                                                                                                                                                                              283 TATAAAACAGGAACCACTAGCACATCTGTTAACTTTACAGATGCCGCGGGTGATCCCATG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity les 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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 ADDRESSEE:
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nucleic acid
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Woodcock, Washburn, Kurtz, Mackiewitz
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US-08-446-855A-1
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                                                                                                                                                                                                                                                     Sequence 1, Application US/08446855A Patent No. 5849573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.18;
Best Local Similarity 46.48;
                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 1888 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDN
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REFERENCE/DOCKET NUMBER: IS:
TELECOMMUNICATION INFORMATION:
                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO ANTI-SENSE: YES
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NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                             APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                       1771 TGAAATCCCATTAGAAGATGCCGCCATGGAATAAAAGCTGATAAATGCTACAATATTAAT 1830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl TITLE OF INVENTION: phosphate synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 TGCAGCAGGTAAATACACTGATGCTGTAACCGTATCTAACCAAGAATTCATGAT 590
                                                                                                                                                                                                                                                                                                                                                                                                 711 AAATATAGATATTTCCATTAAATATGATCCCAGAAAAGATTCGGAGGTTTTTG 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 ACAACTTACTGGTCATGGTTCTTCAGTTTTAGAAGAATTGGTTCAGTTAGTCAAAGATAA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591 TAGAGCCTACGAACAAAACCCACAACATTTTATTGAGGATCTAGAAAAAGTTAGGGTGGA 650
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                 COUNTRY:
                                  STATE:
                                                   CITY: Arlington
                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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STREET: One Liberty Place, 46th floor
                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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22201-4714
                                Virginia
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                                                                  E: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1888;
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 8920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-08-446-855A-1
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Search completed: November 27, 1999, 17:51:25
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Best Local Similarity
Matches 69; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                            7464 ATGCTGGTG 7472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFONMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               7404 TAGATTGTGTTAGTAAAAATGGTAAAATAATTAATTATGCTATATCTGAACATGTTGAAA 7463
                                                                                                                                                                                                                                              7344 TTAGTAAAGATAATCCTGTTGTAATATCAAAATTTATTGAGAATGCTAAAGAAATAGAAA 7403
                                                                                                                     776 TTACTGATG 784
                                                                                                                                                                                                                                                                      656 TTACTGGTCATGGTTCTCAGTTTTAGAAGAATTGGTTCAGTTAGTCAAAGATAAAAATA 715
                                                                                                                                                                                                    716 TAGATATTTCCATTAAATATGATCCCAGAAAAGATTCGGAGGTTTTTGCCAATAGAGTAA 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/01 FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                 Conservative
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7.6;
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Gaps

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9b_htg3:AC008888
9b_p1i:SCYOL087C
9b_in2:AF077591
9b_sts:G41485
9b_htg1:HSDJ81D8
9b_pr1:AB01849
9b_in1:S55234
9b_sts:HUNUT8000
9b_on:SSMSPS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9b_pat: A56812
9b_bal: YPCAF
9b_bal: YPCAF
9b_ba2: AF053947
9b_ba2: AF074611
9b_ba2: AF010149
9b_ba1: S38727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9b_ba1:YE808VANT
9b_ba1:YE527VANT
9b_ba1:YE108VANT
9b_ba1:YE314VANT
9b_ba1:YE314VANT
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gb_pat:A46413
gb_pat:A56793
gb_pat:A56795
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gb_in2:AF167066
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gb_htg1:HSBA425A6
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gb_htg2:AC005918
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gb_ba1:YE96PVANT
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gb_bal:YEPLCRGVHP
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gb_ba1:YEPLCR
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Database length: 2137953050
Search time (sec): 399.000000
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Database: GenEmbl:*
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gb_ba2:AF074612
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-Q=/cgn2_1/USPTO_Spool/US08699716/runat_27111999_151715_6588/app_query.fasta.1
-DB-GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=11.000
-GAPEXT=11.000 -MINMATCH-0.100 -LOOPCL=0.0000 -LOOPEXT=0.000
-OGAPOP-4-500 -OGAPEXT=0.050 -STRART=1 -DTRANS -MATRIX-pam150
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=-escore
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=stat -USER=US08699716
-NCPU=6 -ICPU=3 -WAIT -DM_MEM=28000 -PM_MEM=15000 -THREADS=1
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MODEL=sw.model -DEV=xlp
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.5e-273
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114 | A46411 Sequence 1 from Patent
114 | A46413 Sequence 3 from Patent
114 | A46413 Sequence 3 from Patent
114 | A56793 Sequence 1 from Patent
114 | A56795 Sequence 3 from Patent
11505 | ALI17189 Yersinia pestis pla
11605 | AF074612 Yersinia pestis pla
11765 | AF074612 Yersinia pestis pla
11865 | AF074612 Yersinia pestis pla
1196602 Y.pseudotuberculosis V
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                                                                           2 ! 274829 S.cerevisiae chromosom
! AF077591 Penaeus monodon clone
! G41485 24192 Zebrafish AB Dani
416 ! AL109933 Homo sapiens chrom
! AB018499 Homo sapiens DNA, tri
! AS55234 CAR2=CAMP receptor sub
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81 i AL121749 Homo sapiens chrom
80 i AP000466 Homo sapiens genom
1 AF167066 Crematogaster smithi
2 i AC008888 Homo sapiens chromo
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L30320 Human STS UT8000, seque Z27494 S.scrofa microsatellity AF067896 Drosophila melanogas
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AF074611 Yersinia pestis
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alignment_block:
US-08-699-716A-2 x A56814 (1)
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                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: A56814 from: 1 to: 1530
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                     174 GGKLAAGKYTDAVTVTVSNQ...EFMIRAYEQNPQHFIEDLEKVRVEQLT
                                                                                     105 NNHQFTTKVIGKDSRDFDISPKVNGENLVGDDVVLATGSQDFFVRSIGSK
                                                                                                            124 NNHQFTTKVIGKDSRDFDISPKVNGENLVGDDVVLATGSQDFFVRSIGSK
                                                                                                                                                                                                         74 TIMDNGNIDTELLVGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDG
                                                                                                                                                                                                                                                                                              24 MKKISSVIAIALFGTIATANAADLTASTTATATLVEPARITLTYKEGAPI
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GGKLAAGKYTDAVTVTVSNQGSIEGRIRAYEQNPQHFIEDLEKVRVEQLT
                                                                                                                                                                               TIMDNGNIDTELLVGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDG
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Other publication ZA 9602036 960716
Other publication AU 4951196 961002.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Titball, R.W., William Bennett and Alice, M.
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/protein_id="CAA03423.1"
/db_xref="PID:e1255239"
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/db_xref="GI:3712828"
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KSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK"
a 296 c 311 g 423 t
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KEGAPITIMDNGNIDTELLVGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDGNN
HQFTTKVIGKDSRDFDISPKVNGENLYGDDVVLATGSQDFVRSIGSKGKLLAAGKYT
DAVTVTVSNQGSIEGRIRAYEQNPQHFIEDLEKKVRVEQLTGHGSSVLEELVQLVKDKN
IDISIKYDPRKDSEVFANRVITDDIELLKKILAYFLDEDAILKGGHYDNOLQNGIKRV
KEFLESSPNTQWELRAFMAVMHFSLTADRIDDDILKVIVDSMNHHGDARSKLREELAE
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Other publication
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Sequence 16 from Patent
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SGTINIHDKSINLMDKNLYGYTDEEIFKASAEVKILEKMPQTTIQVDGSEKKIVSIKD
FLGSENKRTGALGNLKNSYSYNKDNNELSHFATTCSDKSRPLNDLVSQXTTQLSDITS
RFNSAIEALNRFIQKYDSVMQRLLDDTSGK"
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publication AU 4951196 961002
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Computer readable copy of sequence [J.kindly submitted by Price, S.
                             J. Bacteriol. 171,
90008806
                                                                       1 (bases 1 to 2100)
Price, S.B., Leung, K.Y., Barve, S.S.
Molecular analysis of lcrGVH, the
                                                                                                                                Yersinia pestis
Bacteria; Proteobacteria;
                                                                                                                                                          LcrG protein; LcrH protein; 75kb virulence plasmid.
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1474...
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1465...
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REFERENCE
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SOURCE
ORGANISM
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US-08-699-716A-2 x A46411
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ORIGIN
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A46411.1
                                                                                                                                                 Quality: 1443.00
Ratio: 4.440
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Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Location/Qualifiers
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Patent: WO 9524475-A 1 14-SEP-1995;
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Titball, R.W., Willia
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BASE COUNT
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LOCUS A46413
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 Similarity: 100.000
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A46413.1
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Bacteria;
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Titball, R.W., Willian
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               Ratio:
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SDKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK"
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               Gaps:
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Titball, R.W., Williamson,
Bennett and Alice, M.
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r publication ZA 9602036
r publication AU 4951196
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LEKMPQTTIQVDGSEKKIVSIKDFLGSENKRTGALGNLKNSYSYNKDNNEISHFATTC
SDKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK"
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US-08-699-716A-2 x A56793 (1)
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LOCUS A56795
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Bacteria;
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                                                                                                                                                                                                              Titball,R.W., Williamson,E.D., Bennett and Alice,M. VACCINES FOR PLAGUE
                                                                                                                                                                                                 Patent: WO 9628551-A 3 19-SEP-1996;
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                                                                                                                                                       publication ZA 9602036 publication AU 4951196
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3 (bases 1 to 70305)
James, K.D., Parkhill, J.,
Direct Submission
                                             2 (bases 1 to 70305)
Baker, S.G. and Mungall, K.
Unpublished
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Ratio: 4.440
nilarity: 100.000
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                                                                                                                  1 (bases 1 to 7030 Karlyshev, A.V. and
                                                                                                                                                                                  Yersinia pestis.
                                                                                                                                                                      Bacteria; Proteobacteria;
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                                                                                                  Unpublished
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AELTAELKIYSVIQAEINKHLSSGGTINIHDKSILMLKNLYGYTDEEIFKASAEYKI
LEKMPQTTIQVDGSEKXIVSIKDFLGSENKRYGALGNLUKNLYGYTDEEIFKASAEYKI
LEKMPQTTIQVDGSEKXIVSIKDFLGSENKRYGALGNLKNSYSYNKDNUELSHFATTC
SDKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK"

184 c 205 g 282 t
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and Wren,
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                   Barrell, B
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-SEP-1999) Yersinia pestis sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBHO 15A E-mail: barrell@sanger ac.uk DNA supplied by Dr. Andrey Karlyshev and Prof. Brendan Wren, [3]. Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, Keppel Diseases, London School of Hygiene and Tropical Medicine, Keppel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/Y_pestis/)
CDS are numbered using the following system eg YPPCP1.01c. YP ()
pestis, PCP1 (plasmid name), .01 (first CDS), c (complementary strand).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tails of Y. pestis sequencing at the Sanger Centre are available the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     putative insertion sequence ISIOO, identical to corresponding CDS from Y.pestis KIM5 pCD1 (EMBL:AF053946, AF074612) (340 aa), fasta scores; opt: 2328 z-score: 3808.9 E(): 0, 100.0% identity in 340 aa overlap. Similar to many others e.g. TRAO_ECOLI (EMBL:X14793), istA, E.coli transposase for insertion sequence element IS21 (390 aa) (33.1% identity in 329 aa overlap). Contains Pfam match to entry pF00239 recombinases, Site-specific recombinases, score 25.70, E-value 4.8e-06. Contains probable helix-turn-helix motif at aa 19-40 (Score 2045, +6.15 SD)"
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88. .1
                                                                                                                                                                                                                                                                                                       SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRSPLHVFVAVLGYSRMLYIEFTDNMR
YDTLETCHRNAFRFFGGVPREVLYDNMKTVVLQRDAYQTGQHRFHPSLWQFGKEMGFS
PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRLRPMGITVDVETANRHGLRWLHDVA
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/db_xref="GI:5832424"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /plasmid="pCD1"
/strain="CO-92 Biovar Orientalis"
/db_xref="taxon:632"
                                                                                                 /note="Pfam match to entry
Site-specific recombinases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/label=YPCD1.01
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/note="YPCD1.01,
/gene="YPCD1.02"
1110. .1889
                                                                                                                                                                                                                                        FCRGVA
                                                                                                                                                                                                                                                                                                                                                                                                        PKYTPRPAVASLLDEYRDYIRQRIADAHPYKIPATVIAREIRDQGYRGGMTILRAFIR
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/הושפהול="הרחו"
                                                                         1110.
                                                                                                                                                                      /gene="YPCD1.01"
                                                                                                                                                                                                                                                                           NQRKHETIQARPCDRWLEEQQSMLALPPEKKEYDVHLDENLVNFDKHPLHHPLSIYDS
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                                                                                                        to entry PF00239 recombinase, 
nmbinases, score 25.70, E-valu
                                                                                                        E-value 4.8e-06"
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/label=YPCD1.04
/protein_id="CAB54881.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="YPCD1 03c, probable transposase remnant, len: 83
/note="YPCD1 03c, probable transposase remnant, len: 83
aa; similar to several e.g. N-terminus of TRR0_ECCLI
(EMBL:X14793), istA, E.coli transposase for insertion
sequence element IS21 (390 aa), similarity is interrupted
by the adjacent IS10 element. The remainder of this CDS
is in YPCD1.97c. This region is also similar to TR:068707
(EMBL:AR053946, AR074612) Y.pestis KIMS putative
transposase in pCD1 (390 aa). Contains probable
helix-turn-helix motif at aa 19-40 (Score 1833, +5.43 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       putative insertion sequence ISIOO, identical to putative insertion sequence ISIOO, identical to corresponding CDS from v.pestis KIM5 pCD1 (EMBL:AF053946, AF074612) (259 aa), fasta scores; opt: 1658 z-score: 2693.4 E(): 0, 100.08 identity in 259 aa overlap. Similar to many others e.g. ISTB_ECOLI (EMBL:X14793), istB, E.col transposase for insertion sequence element IS21 (265 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="identical to Y.pestis KIM5 plasmid pCD1 (EMBL:AF053946) from 46489 to 1955, and to Y.pestis KIM5 plasmid pCD1 (EMBL:AF074612) from 59097 to 14563, except where noted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transposase for insertion sequence element IS21 (265 (47.4% identity in 249 aa overlap). Contains PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                     /note-"YPCD1.04, possible transposase remnant, len: 215 aa; similar to many e.g. TR:Q46612 (EMBL:X78052) Enterobacter agglomerans IS 1222 ORFB (276 aa). Truncate at N-terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="YPCD1.04"
2304. .2948
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HLLHEEKLARHQRKQAMYITMAAFPAVKTFEEDFTFATGAPQKQLQSLKSLSFIERN
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2304. 2948
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/note="PS00017 A
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/db_xref="GI:5832425"
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.2204)
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CDS

misc\_feature

gene gene misc\_feature

06-OCT-1998

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alignment_block:
US-08-699-716A-2 x YPCD1/rev
seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKEFLESSPNTOWELRAFMAVMHFSLTADRIDDDILKVIVDSMNHHGDAR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKY 245
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                                                                                                                                                                                                                                                                                                                                                                                        SKLREELAELTAELKIYSVIQAEINKHLSSSGTINIHDKSINLMDKNLYG
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                                                                                   AIEALNRFIQKYDSVMQRLLDDTSGK 521
     gb_ba2:AF053946
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3600. .4259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yersinia pestis plasmid AF053946
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Hu,P., Elliott,J., McCready,P., Skowronski,I
Kobayashi,A., Carrano,A.V., Brubaker,R. and
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Livermore National Lab, L452, 7000 East Ave., Livermore, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Yop proteins translocation protein K homolog"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="yscK"
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/protein_id="AAC62596.1"
/db_xref_"PID:92996273"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Yop proteins translocation protein M homolog"
/protein_id="AAC62586.1"
/db_xref="PID:92996263"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3193.
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/product="Yop proteins translocation protein I homolog"
/protein_id="AAC62608.1"
/db_xref="pID:g2996285"
                                                                                                               complement(5746.
/gene="yscI"
                                                                                                                                                                                   complement (5746.
                                                                                                                                                                                                      DTYIPQIKQLVNNSIEGLAYDRISVILVPSVDVRQSSHLPRNTSILSIQVSEESKGHL
IGLLSLLILLLPVTNLAQYFWLQRKK"
                                                                                                                                                                                                                                                  SADKEPDKDGKIKLLVEESDVAQAIDILKRKGYPHESFSTLQDVFPKDGLISSPIEEL
ARLNYAKAQEISRTLSEIDGVLVARVHVVLPEEQNNKGKKGVAASASVFIKHAADIQF
                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="yscJ"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5005. .5739)
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                                                                                                                                                            /gene="
                                                                                                                                                                                                                                                                                                translation="MKVKTSLSTLILILFLTGCKVDLYTGISQKEGNEMLALLRQEGL/
                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="yscJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="yscM"
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                                                                                          'codon_start=1
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                                                                                                                                                            Align seg 1/1
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                                                                   8437 MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKY 8486
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                                                                                                             MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKY
                                                                                                                                                                                                                                                                       Quality: 1450.00
Ratio: 4.448
milarity: 100.000
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complement(6937
/gene=""...
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/codor
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/db_xref="GI:2996224"
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FDSFGKRWEAILLQVLEGIKPNESQVGLPYLSELINKELMILLPSNGIVDSLLHNSHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="yscE"
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/gene="ysch"
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/gene="ysch"
                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTQLEEQLHNVETVRSITMQLEMALTKLKKDMMRGGDAKQYQVW
QRESKALESAIAIIHYVAGDLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Yop proteins translocation /protein_id="AAC62550.1" /protein_id="AAC62550.1" /db_xref="FD:92996227" /db_xref="GI:2996227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSNFSGFTKGTDIADLDAVAQTLKKPADDANKAVNDSIAALKDK
PDNPALLADLQHSINKWSVIYNINSTIVRSMKDLMQGILQKFP"
complement(7201. .7401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Yop proteins translocation /protein_id="AAC62549.1" /protein_id="AAC62549.1" /db_xref="GI:2996226" /db_xref="GI:2996226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTFVNGMREQLKT"
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RLSSLMNRGDYASALQQGNKLAYPDLEPWLALCEYRLGLGSALESRLNRLARSQDPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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/protein_id="AAC62548.1"
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/db_xref="GI:2996225"
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GHSLLKEVSDIQKSFKTVKSDLHTKLAVSVDNPNDLMLMQWSLIRITIQEELIAKTAG
                                                                                                                                                                                                                                                                                                                                                                                         complement(7398. .8657)
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Percent Identity:
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F homolog"

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VERSION
KEYWORDS
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LOCUS AF074612
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                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-JUN-1998) Microbiology and Immunology, University of Kentucky, MS415 Medical Center, Lexington, KY 40536-0084, USA Unique identifiers, starting at Y0001, are assigned to each gene of pCD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequencing and analysis of the low-Ca2+-response of Yersinia pestis KIM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 70559)
Perry,R.D., Straley,S.C., Fetherston,J.D.,
Blattner,F.R.
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Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF074612.1 GI:3822037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 70559)
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                                                                                                                                                                              /note="0103; 43 pct identical (0 gaps) to 100 residues
an approx. 200 aa protein GENPEPT: gi|537126, orf_0198
Escherichia coli"
                                                                                                                                                                                                                                                           /gene="Y0001"
57. 368
                                     /translation="MHQQSRGAAGSRTLSLLMRQSGYNVVRWLARRLMRECGLASRQP
GKPRYRGEREVSLASPDLLKRQFKPSEPNRVWSGYISYIKVNGGWCYLALVIDLYSFH
                                                                                                                                                                                                                                                                                              /db_xref="taxon:632"
57. .368
                                                                         /product="unknown"
/protein_id="AAC69758.1"
/db_xref="PID:g3822038"
/db_xref="GI:3822038"
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                          /gene="Y0001"
                                                                                                                                                                                                                                                                                                                                                 /plasmid="pCD1"
                                                                                                                                                                                                                                                                                                                                                                    organism="Yersinia
                                                                                                                                                                                                                                                                                                                                'strain="KIM5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gregor, J. and
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                                                                                                                                                                                                                                                         rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="nuc"
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665. .1033
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NNNYTRLATGAT"
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Tsrfdfsmhvafarslslrhampfllrrailalliqgkofhydplanriqrsitnlai
Ecglateskgsnlstiratralrflselglityqtfydpolgoniftdiftpalfsa
LDVSDVavaaarrsrvewenqqrexqrlprlemdeliakawrfvrerfrsyqterkah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1667. .1741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:3822039"
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                                                                                                       residues of an approx.
lmp2 Xenopus laevis"
                                                                                                                                                           complement(3427. .3645)
/gene="Y0006"
                                                                                                                                                                                               complement(3427.
/gene="Y0006"
                                                                                                                                                                                                                                                                                                                                                                                                                   /product="replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="repA translation
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/note="antisense RNA"
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1171. .1425
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="endonuclease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nuc"
                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Y0005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="tap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="Y0003"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="repA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "translation="MFRKVQYLLRLLLLPCNISAGRCD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'codon_start=1
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/note="Y0010"
7798. . RKK'
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SLDELNVENVSKEIANFYDWLSLVSLPAETAPSYSIYSIG"
5204. 7402
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4758. .5
                                                                                                                                                                                                                                                                                       /product="targeted effector protein"
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WEMDIORSSSECGIFSLALAKKLYIERDSLLKHEDNIKGILSDGENPLPHDKLDPYL
PUTFYKHTQGKKRLNEYLNTNPQGVGTVVNKKNETIVNRFDNNKSIVDGKELSVSVHK
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                                                                                                                                                                                                                 /gene="Y0012"
9858. .10064
                                                                                                                                                                                                                                                         9858
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KHLETLLEVLVTLSQQGQPVSSETYGFLNRLTEAKITLSQQLNTLQQQQESAKAQLSI
LINRSGSWADVARQSLQRFDSTQPVVKFGTEQYTAIHRQMMAAHAAITLQEVSEFTDD
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Orf7 (o142); 31 residues of an approx.
     /translation="MAVGRKNWLFAGSLRAGQRMASILSLLETAKLNGHDPYVWLRDV
LTRLPTWPNSQLNALLPYAENRFS"
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                                                                                                                                                                                                                                                                             KRIAEYKTLLKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ypkA"
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                                                                                                                                                                                                 /gene="Y0012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="yopJ"
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                                                                                                                                                                                                                                                     .10064
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104
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                                                                                                                 JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
     FEATURES
                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                              NID
                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_bal:YPTPIVANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 1450.00
Ratio: 4.448
Percent Similarity: 100.000
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                                                         TITLE
JOURNAL
                                                                                               AUTHORS
                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12640 MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 VKEFLESSPNTQWELRAFMAVMHFSLTADRIDDDILKVIVDSMNHHGDAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIEALNRFIQKYDSVMQRLLDDTSGK 12965
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                             Direct Submission
Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
                 Wuerzburg
                                                                                                                                                                                           Passive immunity to infection with Yersinia spp. mediated by anti-recombinant {\tt V} antigen is dependent on polymorphism of {\tt V}
                                                                                                                                                                                                                                                                                                                                                                    V antigen.
                                                                                                                                                                                                                                                                                                                                                                                        g1405834
X96802.1 GI:1405834
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                                                                                                                                       97162308
                                                                                                                                                                           antigen
                                                                                                                                                                                                                                 Heesemann
                                                                                                                                                                                                                                                                                                                              Yersinia pseudotuberculosis
                                                                                               Roggenkamp, A.
                                                                                                                                                                                                                                                   Roggenkamp, A., Geiger, A.M., Leitritz, L., Kessler, A.
                                                                                                                                                                                                                                                                                             Yersinia.
                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                  Yersinia pseudotuberculosis.
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.pseudotuberculosis V
                                                                                                                 (bases 1 to 981)
                                                                                                                                                                                                                                                                       (bases 1 to 981)
                                                                                                                                                       Immun. 65 (2),
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/gene="yoph"
/note="Y0013"
10347. .11753
/gene="yoph"
/codon_start=1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      981
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SOURCE
ORGANISM
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LOCUS YEPLCRGVHP
                                                                                                                                                                                                                                       seq_name: gb_ba1:YEPLCRGVHP
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                                                                 VERSION
                                                                                                           ACCESSION
                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: YPTPIVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-699-716A-2 x YPTPIVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                    446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKEFLESSPNTQWELRAFMAVMHFSLTADRIDDDILKVIVDSMNHHGDAR 345
                                                                                                                                                                                                                                                                                                                                                                                           GNLKNSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKY
                                                                                                                                                                                                                                                                                                          AIEALNRFIQKYDSVMQRLLDDTSGK 521
                                                                                                                                                                                                                                                                                                                                                                         GNLKDSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTDEEIFKASAEYKILEKMPQTTIQEGETEKKIVSIKNFLESEKKRTGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTDEEIFKASAEYKILEKMPQTTIQVDGSEKKIVSIKDFLGSENKRTGAL 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKLREELAELTAELKIYSVIQAEINKHLSSGGTINIHDKSINLMDKNLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKLREELAELTAELKIYSVIQAEINKHLSSSGTINIHDKSINLMDKNLYG
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                                                                                                                                                                                                                                                                                  AIEALNRFIQKYDSVMQRLLDDTSGK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                         Yersinia pseudotuberculosis V-antigen (LcrG, LcrV, LcrH) genes, M57893
Yersinia pseudotuberculosis (strain YPIII (pIB1) DNA
Yersinia pseudotuberculosis
                                          V-antigen.
                                                                 M57893.1 GI:155456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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MPQTTIQEGETEKKIVSIKNFLESEKKRTGALGNLKDSYSYNKDNNELSHFATTCSDK
SRPLNDLVSQKTTQLSDITSRENSAIEALNRFIQKYDSVMQRLLDDTSGK"
41 a 174 c 191 g 275 t
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4.390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Yersinia pseudotuberculosis"
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BASE CO
alignment_scores:
    Quality:
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                                                                                                          COUNT
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Baeckman,A., Boelin,I. and Wolf-Watz,H.
Analysis of the V antigen lcrGVH-yopBD Operon of Yersinia
pseudotuberculosis: Evidence for a regulatory role of LcrH and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.
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                                                                                                          D
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EPRFPFHAAECLLQKGELAEAESGLFLAQELIADKPEFKELSTRVSSMLEAIKLKKEM
EHECVDNP"

450 c 485 g 552 t
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252...2
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241. .24
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                                                                                                                                                                                                                                                                                                                                                               1546. .2052
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                                                                                                                                                                                                                                                                                                 /evidence=experimental
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQRLLDDTSGK'
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1418.00

Length:

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AUTHORS
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US-08-699-716A-2 x
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ORGANISM
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                                                                                                                                                                                                            Homology between virf, the transcriptional activator of the Yersinia virulence regulan, and AraC, the Escherichia coli J. Bacteriol. 171 (1), 254-262 (1989)
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                                                                      Wattiau, P. and Cornelis, G.R. SycE, a chaperone-like protein in Ohe secretion of YopE
                                                                                                                                                                                                                                                                                                                                                                                     M22781 U08222 Z18539 U94827
g4324323
AF102990.1 GI:4324323
                                                                                                                                                                                                                                                                                                                                                                                                                              AF102990 69673 bp DNA circular BCT 18-MAY-1999 Versinia enterocolitica plasmid pYve227, complete sequence. AF102990 AF05498 AF054979 AF054980 AF054981 AF080156 Z69926 L06216 AF080155 AF022645 AF050104 AF054977 AF033863 U02499 U08019 U21297
Woestyn, S., Allaoui, A., Wattiau, P. and YscN, the putative energizer of the Yer
                                             Mol. Microbiol. 8 (1), 123-131 93268087
                                                                                                                                                                                 2 (bases 15074 to 15994)
Hakansson, S., Bergman, T.,
                                                                                                                                                                                                                                                                                                                                             Yersinia enterocolitica
Yersinia enterocolitica
                                                                                                                                 93114907
                                                                                                                                                                         Wolf-Watz, H
                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                           YopB and YopD constitute a novel class of infect. Immun. 61 (1), 71-80 (1993)
                              (bases 23950 to 25269)
                                                                                                                 (bases 45325 to 45717)
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  Yersinia
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  Yop secretion
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Direct Submission
Submitted (30-OCT-1998) Microbial Pathogenesis Unit, Christian de Duve Institute of Cellular Pathology and Faculte de Medecine.
Universite Catholique de Louvain, Av. Hippocrate 74.49, Brussels 1200, Belgium
On May 18, 1999 this sequence version replaced gi:3411136 gi:3411139 gi:3411137 gi:3603360 gi:1524380 gi:15536 gi:3603357 gi:2738986 gi:2944089 gi:3411138 gi:3108216 gi:437201 gi:497215 gi:885971 gi:155526 gi:483322 gi:48593 gi:2733421.
Location/Qualifiers
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10 (bases 22612 to 22890)
11 (bases 22612 to 22890)
11 (arte, M., Sory, M.P., Boland, A., Boyd, A.P., Lambermont, I. and Cornelis, G.R.
12 (arte, M., Sory, M.P., Boland, A., Boyd, A.P., Bornelis, G.R.
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Boyd, A.P., Sory, M.P., Iriarte, M. and Cornelis, G.R.
Heparin interferes with translocation of Yop proteins into HeLa
cells and binds to LcrG, a regulatory component of the Yersinia
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Iriarte,M., Lambermont,I.,
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                                                                                                             SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_
                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6026 YTDEEIFKASAEYKILEKMPQTTIKEGETEKKIVSIKNFLESENKRTGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNLKNSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNS
                                                                                                                                                                                                                                                                                                                   X96801
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CDS

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Quality:
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4.372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSETIWLEPSSQKTVYLQIKNTSDKNMLGLAPKITKAVQDKGYTVTSSPEDAHYWIQA
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Gaps: 0
Percent Identity: 95.356
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CDS

gene

Percent Similarity:

alignment\_block: US-08-699-716A-2 x AF102990/rev (4) from: Н to: 69673

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gene

CDS

496 AIEALNRFIQKYDSVMQRLLDDT 518 AIEALNRFIQKYDSVMQRLLDDT 5904 GNLKDSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNS

495

5977

seq\_name: gb\_ba1:YE96PVANT

REFERENCE g1405830 X96801.1 V antigen. Yersinia enterocolitica. Yersinia enterocolitica Yersinia Bacteria; Proteobacteria; E96PVANT .enterocolitica V antigen GI:1405830 1 to 975) 975 bp gamma subdivision; Enterobacteriaceae; gene, strain Y-96-P.

CDS gene

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BASE COUNT
ORIGIN
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MEDLINE
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: YE96PVANT from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-699-716A-2 x YE96PVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
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                  446 GNLKNSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNS
                                                                                                                       396
                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                               201
                                                                                                                                                                                                       346
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                                                                                                                                                                                                                                                                                                                                                246 DPRKDSEVFANRVITDDIELLKKILAYFLPEDTILKGGHYDNQLQNGIKR
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                                                                                                                                                                                                                                                                    VKEFLESSPNTQWELRAFMAVMHFSLTADRIDDDILKVIVDSMNHHGDAR
GNLKDSYSYNKDNNELSHLGTTCSDKSRPLNDLVSQKTTQLSDITSRFNS
                                                                                                                                                           YTDEEIFKASAEYKILEKMPQTTIQVDGSEKKIVSIKDFLGSENKRTGAL 445
                                                                                                                                                                                                                                                                                                                             DPQKDSEVFADRVITDDIELLKKILAYFLPEDAILKGGHYDNQLQNGIKR
                                                                               YTDEEIFKASAEYKILEKMPQTTIKEGETEKKIVSIKNFLESENKRTGAL
                                                                                                                                                                                                                                             VKEFLESSPNTQWELRAFMAVMHFSLTADRIDDDILKVIVDSMNHHGDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 1379.00
Ratio: 4.323
nilarity: 98.762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Wuerzburg, Wuerzburg, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (22-MAR-1996) A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Passive immunity to infection with Yersinia spp. mediated by anti-recombinant V antigen is dependent on polymorphism of \boldsymbol{V}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roggenkamp, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heesemann,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roggenkamp, A., Geiger, A.M., Leitritz, L., Kessler, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335
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SRPLMBUVSQKTTQLSDITSRENSAIEALNRFIQKYDSVMQRLLDDTR"
35 a 177 c 194 g 269 t
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/db_xref="taxon:630"
1. .975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Yersinia enterocolitica (type 0:9)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="taxon:34055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 (2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 93.808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446-451 (1997)
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Josef-Schneider Strasse 2, 97080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Gaps:
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300
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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LOCUS YE808VANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_ba1:YE808VANT
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                                                                              Align seg 1/1
                                                                                                                     US-08-699-716A-2 x YE808VANT
                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
196 MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 AIEALNRFIQKYDSVMQRLLDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIEALNRFIQKYDSVMQRLLDDT
                                                                                                                                                                            Quality: 1378.00
Ratio: 4.320
milarity: 98.762
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x96798.1
V antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and University of Wuerzburg, Josef-Schneider Strasse 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Passive immunity to infection with Yersinia spp. mediated by anti-recombinant {\bf V} antigen is dependent on polymorphism of {\bf V}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia enterocolitica.
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170 c 192 g 274 t
                                                                                                                                                                                                                                                                                                                                                        EFLESSPNTQWELRAFMAVMHFSLTADRIDDDILKVIVDSMNHHGDARSKLREELAEL
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/strain="8081"
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jb_est28:AI518356

jb_est23:AI133907

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jb_est19:AA263871

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gb_est28:AI531330
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-Q=/Cgn2_1/USPT0_spco1/USO8699716/runat_27111999_151715_6579/app_query.fasta.
-Q=/Cgn2_1/USPT0_spco1/USO8699716/runat_27111999_151715_6579/app_query.fasta.
-DB=EST -QFMT=fastap -SUFFIX=rst -GAPOP=11.000 -GAPEXT=11.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -START=1 -DTANS -MATRIX=PDMT150
-TRANS-human40.cdi -LIST45 -DOCALIGN=200 -THR_SCORE=escore
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=stat -USER=US08699716
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AA484400 UT-M-BH1-aks-d-03-0-U
AA484400 LD364540 UT-M-BH1-aks-d-03-0-U
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                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases I to 621)
                                                                                                                                                                                                                                                        AI531330 621 bp mRNA EST 18-MAR-1999 AI531330 EST ESD02320.5prime SD Drosophila melanogaster Schneider L2 cell cutture pOT2 Drosophila melanogaster cDNA clone SD02320 5prime similar to L42311; shn FBgn0003396 PID:g845332 SPTREMBL:Q24605, mRNA sequence
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Dictyostelium discoideum
Harvey,D., Hong,L., Evans-Holm,M., Brokstein,P., Lewis,S. and Rubin,G BDGP/HHMI Drosophila EST Project
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Email: d402hu@sakura.cc.tsukuba.ac
PROJECT - Dictyostelium discoideum
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[ (bases 1 to 571)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATANAADLTASTTATATLVEPARITLTYKEGAPITIMDNGNIDTELLVGT 89
                   G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                         Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J.,
Barokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi
                                                                                                                                                                                                                                                                                                                                                                                                                            AA391919 442 bp mRNA
AA391919 10 LD10828.5prime LD Drosophila melanogaster embryo BlueScript
LD10828.5prime, mRNA sequence.
                                                                                                                                                                                                                                        Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 442)
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On Mar 10, 1998 this sequence version replaced gi:2948191.
                                                                                                                                                                                                                                                                                                                                                                                                                  g2044894
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                                                                                                     Contact: Harvey, D.
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http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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172 c 133 g 100 t
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/lab_host="DH5-alpha"
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77.273
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/db_xref="taxon:7227"
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                                                                                                                                         this sequence version replaced gi:1400810
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28.409
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SOURCE
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    BASE COUNT
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                                                                                                                                                                                3-3-10 Ten-nodai, Tsukuba, Ibaraki
Email: d402hu@sakura.cc.tsukuba.ac.
PROJECT = 'Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                   Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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99156227
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136 c 130 g 79 t
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Location/Qualifiers
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/db_xref="taxon:7227"
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83 c 62 g 206 t
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                                                                                                     /strain="AX4"
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alignment_block:
US-08-699-716A-2 x AA538585
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Quality:
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LOCUS AA538585
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Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokstein,P., Lewis,S. and Rubin,G.M.
BGGP/HHMI Drosophila EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2285101.
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LD18150.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD18150 5prime, mRNA sequence.
AA538585
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Plate: 181 row: E column: 2
High quality sequence stop: 419.
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                                                                                                                                                                                              /note="Organ: embryo; Vector: BlueScript SK; Site_1: EcoRI; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at ECORI and XhoI in BlueScript SK(+/-)"

183 c 166 g 110 t 1 others
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3.500
88.000
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3.208
85.714
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/lab_host="SOLR"
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Identity: 53.571
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SOURCE
ORGANISM
LOCUS AI182515 440 bp mRNA EST 08-OCT-19: DEFINITION ue21g12.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
                         seq_documentation_block:
LOCUS AI182515
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LOCUS AA201964
                                                                                    seq_name: gb_est24:AI182515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
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                                                                                                                                   109 GHHGHHHHHHTSANVDGLDTHNLKLPA 136
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                                                                                                                                                      2 GHHHHHHHHHHSSGHIDDDDDKHMKKISS 29
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Ratio:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 437)

1 (bases 1 to 437)

Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,

Brokstein,P., Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LD05053.5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD05053 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 50 row: E column: 5
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of California Berkeley 539 LSA, Berkeley, CA 94720-3200, Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G. M. Rubin-Molecular and Cell Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Harvey, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 18, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA201964.1 GI:1797767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                        AA201964 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: embryo; Vector: BlueScript SK; Site_1:
EcoRI; Site_2: XhoI; Constructed using Stratagene ZAP-cI
Synthesis kit. Oligo dT-primed and directionally cloned
ECORI and XhoI in BlueScript SK(+/-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="LD Drosophila melanogaster embryo BlueScript"/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="BDG_EST:BDcln004432"
/db_xref="taxon:7227"
/clone="LD05053"
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3.125
85.714
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cloned at
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REFERENCE
AUTHORS
    seq_name: gb_est14:AA441519
                                                                                                                                                                         alignment_block:
US-08-699-716A-2 x AI182515/rev (6)
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ORIGIN
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                                                                                                                                   Align seg 1/1 to reverse of: AI182515
                                                                                                                                                                                                                                               Percent Similarity:
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                 ИНИННИННОSSHREKGERERER 113
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g3733153
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Ratio:
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI182515.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jan 14, 1998 this sequence version replaced gi:2754392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

94 c 104 g 151 t
                                                                                                                                                                                                                                             75.00
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/sex="female"
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/clone="IMAGE:1481062"
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/strain="C57BL"
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                                                                                                              ACCESSION
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seq_documentation_block:
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US-08-699-716A-2 x AA441519
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                                                                                                                                                                                                                                                                                                                                                                    GHHHHHHHHHHSSGHIDDDDKHMKKISS
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Ratio:
                                                                                                                           AA439056 499 bp mRNA EST 28-NOV-1998
LD13501.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA cione LD13501 5prime, mRNA sequence.
AA439056
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1 (bases 1 to 491)
Harvey,D., Hong,L., Evans.Holm,M., Pendleton,J., Su,C., Brokytein,P., Levis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1395398.
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LD16485.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD16485 5prime, mRNA sequence.
AA441519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 164 row: H column: 1
High quality sequence stop: 363.
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                        fruit fly.
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155 c 138 g 94 t
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3.125
85.714
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/db_xref="BDGP_EST:BDc1n015696"
/db_xref="taxon:7227"
/clone="LD16485"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
melanogaster
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                                                                             GI:2150937
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Gaps: 0
Percent Identity: 53.571
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REFERENCE
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AUTHORS
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    Quality:
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US-08-699-716A-2 x AA439056
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                                         Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 506)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
Brokstein, P., Lewis, S. and Rubin, G.M.
Brokstein, P., Lewis, S. and Rubin, G.M.
Dogp/HHMI Drosophila EST Project
Unpublished (1997)
On Jan 5, 1998 this sequence version replaced gi:2581344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:13934
                                                                                                                                                                                                                                                                                                                                                                             AA735384 506 bp mRNA EST 27-N LD21220.5prime LD Drosophila melanogaster embryo p072 melanogaster cDNA clone LD21220 5prime, mRNA sequence. AA735384
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University of Callifornia Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
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1 (bases 1 to 499)
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High quality sequence stop: 427.
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Plate: 135 row: A column: 1
Contact: Harvey,
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154 c 145 g 93 t
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3.125
85.714
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
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/db_xref="BD6P_EST:BDc1n012732"
/db_xref="taxon.7227"
/clone="LD13501"
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Gaps: 0
Percent Identity: 53.571
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LOCUS AA948995
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1 (bases 1 to 523)

1 (bases 1 to 523)

1 (bases 1, Evans-Holm,M., Pendleton,J., Su,C., Brokstein,P., Lewis,S. and Rubin,G.M.

BDGP/HIMI Drosophila EST Project

Unpublished (1997)
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AA948995
                                                                                                                                 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 277 row: B column: 10
High quality sequence stop: 512.
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University of California Berkeley
539 LSA, Beckeley, CA 94720-3200, USA
Fax: 510 643 9947
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University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                           Contact: Harvey, D.
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163 c
/clone="LD27722"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
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XhoI; Sized fractionated cDNAs were directly ligated into
poT2.
                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                               Location/Qualifiers
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/lab_host="XL1 Blue"
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/db_xref="taxon:7227"
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/sex="male and female"
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Gaps: 0
Percent Identity: 53.571
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LOCUS AA820589
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Percent Similarity:
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1 (bases 1 to 554)
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AA820589
   Quality:
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Plate: 243 row: H column: 10
High quality sequence stop: 448.
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G. M. Rubin-Molecular and Cell Biology
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171 c
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//dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/lab_host="XL1 Blue"
/note="Organ: embryo; Vector: poT2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into poT2. "
                                                                                                                                                                                                                                  /note="Organ: embryo; Vector: pOT2;
XhoI; Sized fractionated cDNAs were
pOT2. "
                                                                                                                                                                                                                                                                                                                            /clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/map="11 q13.4-q23.2"
/clone="LD24394"
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Gaps: 0
Percent Identity: 53.571
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directly ligated into
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REFERENCE
AUTHORS
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ORGANISM
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US-08-699-716A-2 x AA264342 (1)
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US-08-699-716A-2 x AA820589
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ORIGIN
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LOCUS AA264342
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Percent Similarity:
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                                                                               Align seg 1/1 to: AA264342 from: 1
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JOURNAL
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112 GHHGHHHHHHTSANVDGLDTHNLKLPA 139
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                     2 GHHHHHHHHHHSSGHIDDDDKHMKKISS 29
                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
plate: 75 row: G column: 10
High quality sequence stop: 499.
Location/Qualifiers
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Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophia EST Project
Unpublished (1997)
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LD07582.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD07582 5prime, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of California Berkeley 539 LSA, Berkeley, CA 94720-3200,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G. M. Rubin-Molecular and Cell Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Harvey, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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                                                                                                                                                                                                                                                                                                                                    QJ
                                                                                                                                                                                                                                                                                                                               /note="Organ: embryo; Vector: BlueScript SK; Site_1: EcoRI; Site_2: KhOI; Constructed using Stratagene ZAP-cI Synthesis kit. Oligo dT-primed and directionally cloned EcoRI and XhoI in BlueScript SK(+/-)"

175 c 155 g 103 t
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3.125
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDcln006957"
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85.714
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Gaps: 0
Percent Identity: 53.571
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Percent Identity: 53.571
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seq_documentation_block:
LOCUS AI260971
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US-08-699-716A-2 x AA264985
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ORIGIN
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                                                                ACCESSION
                                                                                                             DEFINITION
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                       VERSION
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KEYWORDS
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JOURNAL
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101 GHHGHHHHHHTSANVDGLDTHNLKLPA 128
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                                                            AI260971 572 bp mRNA EST 17-NOV-1998
LP05026.5prime LP Drosophila melanogaster larval-early pupal pOT2
Drosophila melanogaster cDNA clone LP05026 5prime, mRNA sequence.
AI260971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 565)
Harvey D Hong I Francische M Doddloto I G. G.
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LD08662.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD08662 5prime, mRNA sequence.
AA264985
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539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
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BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                         g3868496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 86 row: F column: 2
High quality sequence stop: 460.
Location/Qualifiers
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                  AI260971.1
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3.125
85.714
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173 c 159 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
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/db_xref="taxon:7227"
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                    GI:3868496
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Gaps: 0
Identity: 53.571
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COMMENT
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                                                                              Align seg 1/1
                                                                                                                      US-08-699-716A-2 x AI260971
                                                                                                                                                                                 Percent Similarity:
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100 GHHGHHHHHHTSANVDGLDTHNLKLPA 127
                                        N
                                     GHHHHHHHHHSSGHIDDDDKHMKKISS
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BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Aug 21, 1998 this sequence version replaced.
                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AL031765
Plate: 50 row: C column: 2
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University of Callifornia Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins. Pterygota; Neophera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 572)
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Location/Qualifiers
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ligated into pOT2. Plasmid cDNA library.
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/db_xref="taxon:7227"
/clone="LP05026"
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/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
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N_Geneseq_36:V41600
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Query length:
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Database sequences: 311585
Database length: 125096042
Search time (sec): 73.360000
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_Geneseq_36:T04223
_Geneseq_36:V41595
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-Q=CG972_1/USPTO_SpOol/US08699716/runat_27111999_151715_6614/app_query.fasta.
-QAPEXT=11.000
-QAPEXT=0.000 -MINMATCH=0.100 -LOODCL=0.000 -LOODEXT=0.000
-QGAPEXT=0.050 -START=1 -DTRANS -MATRIX=pam150
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=escore
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=stat -USER-US08699716
-NCPU=6 -ICPU=3 -WAIT -DM_MEM=28000 -PM_MEM=15000 -THREADS=1
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6:Q92818
6:V41598
6:V41599
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6:Q81500
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6:V30596
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6:T33362
6:T33359
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6:Q95175
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Y. pestis lcrV (V antigen) gene
Y. pestis lcrV (V antigen) gene
Partial LcrV (V antigen) gene
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                            residia postis V antigen and F1 antigen or their protective peptiopic parts - useful in vaccine for protection against plague S Claim 41; Page 65-69; 98pp; English.

Claim 41; Page 65-69; 98pp; English.

C A gene fusion (T38249) comprises coding sequences for the Yersinia pestis F1 antigen (see also T38248) including the signal sequence and for the Y. pestis V antigen (see also T38243), joined by a Sequence encoding a 6-amino acid peptide linker. It was obtd. by PCR amplification of the individual genes using primers (see also T38245) based on the genes and including linker sequences. The gene fusion (see also T38256) can be used to produce F1/V fusion protein (W01044) in transformed cells, esp. gut-colonising organisms, to induce an immune response against Y. pestis, the sequence 1530 BP; 499 A; 296 C; 312 G; 423 T;
                                                                                                                                                                                                                     Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MINA ) UK SEC FOR DEFENCE.
Bennett AM, Leary SEC, Oyston PCF, Titball RW, WPI; 96-433824/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1995; GB-005059
15-SEP-1995; GB-018946
05-DEC-1995; GB-024825
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19-SEP-1996.
13-MAR-1996; G00571.
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                 124 NNHQETTKVIGKDSRDFDISPKVNGENLVGDDVVLATGSQDFFVRSIGSK
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seq_documentation_block:
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13-MAR-1995; GB-005059.
15-SEP-1995; GB-018946.
05-DEC-1995; GB-024825.
(MINA) UK SEC FOR DEFENCE.
Bennett AM, Leary SEC, Oys
WPI; 96-433824/43.
Versinia pestis V antigen and Fl antigen or their protective epitopic parts - useful in vaccine for protection against plague Disclosure; Page 51-55; 98pp; English.

A gene fusion (T38256) comprises coding sequences for the Yersinia pestis Fl antigen (see also T38244) (without the signal sequence) and for the Y. pestis V antigen (see also T38243), joined by a sequence encoding a 6-amino acid peptide linker. It was obtd. by TCR amplification of the individual genes using primers (see also T38245) based on the genes and including linker sequences. The genes also T38245) can be used to produce F1/V fusion protein (w01045) in transformed cells, esp. gut-colonising
                                                                                                                                                                                                                                                                                                                                                              Chimeric
Chimeric
Key
                                                                                                                                                                                                                                                                                                                                                                                           Plague; vaccine; genetic immunisation; Fl antigen; cafl; ds.
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Y. pestis F1/V antigen gen
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452. .472
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/note= "bases 452-472
from PCR primers"
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                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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US-08-699-716A-2
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T04222;
18-APR-1996 (first entry)
Partial LcrV (V antigen) gene
LcrV; V antigen; virulence; p
                                                                                                                                                                            _documentation_block:
W09524475-A1.
11-SEP-1995.
06-MAR-1995; G00481.
08-MAR-1994; GB-004577.
(MINA) UK SEC FOR DEFENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organisms, to induce an immune causative organism of plague. Sequence 1462 BP; 476 A;
                                                                                                     Yersinia pestis
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4.254
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1. .990
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Gaps:
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seq_name: N_Geneseq_36:T38242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA expressing versinia pestis V antigen - useful in protection against plague or all or parenteral vaccines for protection against plague protective epitopic ps Claim 6; Page 11-13; 25pp; English.

CC T0422-23 are DNA sequences (lcrV) encoding all or a protective epitopic part of the mature V protein with maltose binding protein or expressed as a fusion protein with maltose binding protein or glutathione- S-transferase in 3 different plasmid vectors. Y pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (LcrV) is an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/ peptide are useful in vaccines to protect against plague.

So Sequence 1014 BP; 346 A; 181 C; 201 G; 286 T;
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                                 misc_feature
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Y. pestis lc
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                                                                                              Yersinia pestis
                                                                                                           F1 antigen;
                                                                                                                            Plague; vaccine; genetic immunisation;
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                                                                                                                                             -DEC-1996 (first entry) pestis lcrV (V antigen)
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Ratio: 4.440
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1. .6
/*tag=
                                                                                                strain GB
                                                                           Location/Qualifiers
 /note=
                                                                                                                                                                                                DNA; 1014
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"vector pMAL-p2 or pMAL-c2-derived bases"
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                                                                                                                            V antigen; lcrV;
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alignment_scores;
Quality: 1443.00
Ratio: 4.440
Percent Similarity: 100.000
seq_documentation_block:
ID T38243 standard; DNA; 1014
                                                                          seq_name: N_Geneseq_36:T38243
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US-08-699-716A-2 x T38242
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CC AlcrV gene sequence (T38242) codes for the Yersinia pestis V CC antigen (W01040), which is capable of evoking protective immune CC composes in animals. The gene was amplified from Y. pestis CC DNA by PCR using primers (T38250-51) homologous to the 5' and 3' CC ends of the gene. The gene was inserted into vector pMAL-p2, CC pMAL-c2 or pEEX-5X-2 (see also T38243) to allow prodn. of C recombinant V antigen for use in vaccines against plague.

CC Expression in gut-colonising organisms and attenuated Salmonella CC typhi allows prodn. of live vaccines. F1/V antigen fusions were CC also created (see also T38249 and T38256). The gene can itself be CC considered the colonism of the production of the colonism of the colonism of the pertical colonism of the coloni
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Bennett AM, Leary SEC, Oy
WPI; 96-433824/43.
P-PSDB; W01040.
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13-MAR-1995; GB-005059.
15-SEP-1995; GB-018946.
05-DEC-1995; GB-024825.
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e 1014 BP; 347 A;
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/note= "base 1006 is altered
second in-frame stop codon"
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alignment_block:
US-08-699-716A-2 x T38243
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The gene was amplified from Y. pestis or esponses in animals. The gene was amplified from Y. pestis on a standard standa
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19-SEP-1996.
13-MAR-1996; G00571.
13-MAR-1995; GB-005059.
15-SEP-1995; GB-018946.
05-DEC-1995; GB-024825.
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28-DEC-1996 (first entry)
7. pestis lcrV (V antigen) gene.
71-2006: vaccine; genetic immunisation; V antigen; lcrV;
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Bennett AM, Leary SEC, Oy
WPI; 96-433824/43.
P-PSDB; W01041.
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Similarity:
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Percent Identity: 99.692
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alignment_block:
US-08-699-716A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA expressing Versinia pestis V antigen - useful in or parenteral vaccines for protection against plague claim 6; Page 15-16; 25pp; English.

Claim 6; Page 15-16; 25pp; English.

T04222-23 are DNA sequences (lcrV) encoding all or a protective epitopic part of the mature V protein of Versinia pestis. The protein was expressed as a fusion protein with maltose binding protein or glutathione- S-transferase in 3 different plasmid vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (LcrV) is an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/ peptide are useful in vaccines to protect against plague.

Sequence 1014 BP; 343 A; 185 C; 204 G; 282 T;
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14-SEP-1995.
06-MAR-1995; G00481.
08-MAR-1994; GB-0045
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Key
cds
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(MINA ) UK SEC FOR DEFENCE.
Leary SEC, Titball RW, Wi
WPI; 95-328268/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial LcrV (V antigen) gene of Y. LcrV; V antigen; virulence; plague;
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Claim 8; Page 53; 75pp; English.
This is the nucleotide sequence of a Yersinia pestis F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.
Sequence 510 BP; 153 A; 114 C; 106 G; 137 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HESK-) HESKA CORP.
Haanes EJ, Osorio JE, Thomas RE,
WPI; 98-333331/29.
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04-DEC-1997; U22617.
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Nucleotide sequence of F1 antigen nYpF1(b)sec544.
F1 antigen; plasmid; vaccine; plague; ds.
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Yersinia pestis cafl (F1) antigen in plasmid pFORF1b.
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bubonic plague; pne
Yersinia pestis.
Key Loc
cds 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA constructs capable of transforming microorganisms - which can used as live or attenuated vaccines which induce an immune respon against Yersinia pestis, at mucosal surfaces. Disclosure; Page 19-20; 27pp; English. The sequence represents the plasmid pFORF1b including the entire v. pestis cafl (F1) antigen gene having a 5' tail including a Sac restriction site, and up to TATAG downstream of the cafl ORF. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, and are parenterally and orally active vaccines offering protection against bubonic and pneumonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MINA) UK SEC FOR DEFENCE. Howells A, Leary SEC, Oys WPI; 95-246396/32. P-PSDB; R76528.
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pneumonic plague; ds.
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seq_documentation_block:
ID V41596 standard; DNA;
AC V41596;
DT 26-OCT-1998 (first e
DE Nucleotide sequence o
KW F1 antigen; plasmid;
OS Yersinia pestis
FH Key
FT CDS /*tag
FT CDS /*tag
FT CDS /*tag
FT CDS 11-JUN-1998.
PF 04-DEC-1997; U22617.
PR 04-DEC-1996; US-7671.
PA (HESK) HESKA CORP.
PB 1-Haanes EJ, Osorio JE
DR WPI; 98-33331/29.
DR P-PSDB; W59783.
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US-08-699-716A-2 x V41594
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                11-JUN-1998.

04-DEC-1997; U22617.

04-DEC-1996; US-767115.

(HESK-) HESKA CORP.

Heanes EJ, Osorio JE, Thomas RI

WPI; 98-33331/29.
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04-DEC-1997; UZ2617.

04-DEC-1996; US-767115.

(HESK-) HESKA CORP.

Haanes EJ, Osorio JE, Thomas R

WPI; 98-333331/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 8; Page 51; 7,5pp; English.

This is the nucleotide sequence of a Yersinia pestis F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.

Sequence 544 BP; 164 A; 120 C; 114 G; 146 T;
                                                                                                                                                                                                              26-OCT-1998 (first entry)
Nucleotide sequence of F1 antigen nYpF1sec510.
F1 antigen; plasmid; vaccine; plague; ds.
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Similarity:
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seq_documentation_block:
ID T38248 standard; DNA;
AC T38248;
DT 28.DEC-1996 (first e
DE Y. pestis F1 antigen
KW Plague; vaccine; gene
KW Vantigen; ds.
OS Yersinia pestis strai
FH Key Locat
FT signal_peptide 29.
FT mat_peptide 92.
FT mat_peptide 92.
FT W09628551-A1.
PD 19-SEP-1996; G00571.
PF 13-MAR-1995; GB-0050;
PR 13-MAR-1995; GB-0050;
PR 13-MAR-1995; GB-0050;
PR 13-MAR-1995; GB-0048;
PR 05-DEC-1995; GB-0048;
PR WDI; 96-433824/43.
PT Yersinia pestis V an-
PT epitopic parts - use
PS Claim 41; Page 61-62
CC A DNA sequence (T382
CC A DNA sequence (T382
CC and the resulting pla
CC strains of the composition
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13-MAR-1995; GB-005059.

15-SEP-1995; GB-018946.

05-DEC-1995; GB-024825.

(MINA ) UK SEC FOR DEFENCE.

Bennett M., Leary SEC, Oys:

WPI; 96-433824/43.
                                             epitopic parts - useful in vaccine for protection against plague Claim 41; Page 61-62; 98pp; English.

A DNA sequence (738248) comprises the cafl gene, including the signal sequence, coding for the F1 antigen (W01043) of Yersinia pestis. It was obtd. by PCR amplification (see also T38257-58) of Y. pestis DNA. The PCR product was cloned into plasmid pBKCMV and the resulting plasmid (pF1AB) was used to transform E. coli we have a comparable of the product was considered by i.m. injection, and the product was considered by i.m. injection, and the product was used to transform E. coli we have a considered by i.m. injection, and the product was considered by i.m. injection, and injection.
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This is the nucleotide sequence of a Yersinia pestis F1 antigen, us in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable o protecting an animal from contracting plague.

Sequence 544 BP; 166 A; 118 C; 112 G; 148 T;
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    vaccines comprising gut colonising organisms transformed with the
                                 induced an immunoglobulin response to F1 in BALB/c mice
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6
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alignment_scores:
    Quality:
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Percent Similarity:
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US-08-699-716A-2 x T38248 (2)
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                    alignment_block:
US-08-699-716A-2 x V41609 (1)
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Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
                                                                                                                               Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 8: Page 64; 75pp; English.
This is the nucleotide sequence of a Yersinia pestis Fl antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.

Sequence 447 BP; 133 A; 102 C; 95 G; 117 T;
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Sequence 547 BP; 165 A;
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11-JUN-1998.
04-DEC-1997; U22617.
04-DEC-1996; US-767115.
                                                                                                                                                                                                                                                                                                                                                                                           Yersinia pestis.
Key
                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1998 (first entry)
Nucleotide sequence of F1 antigen nYpF1mat447.
F1 antigen; plasmid; vaccine; plague; ds.
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Haanes EJ, Osorio JE, Thomas RE;
WPI; 98-333331/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                             V41609;
26-OCT-1998
                                                                                                                                                                                                                                                    P-PSDB; W59788.
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seq_documentation_block:
ID V41600 standard; DNA;
AC V41600;
DT 26-OCT-1998 (first e
DE Nucleotide sequence c
KW F1 antigen; plasmid;
OS Yersinia pestis. Locat
FT CDS 7. .4
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US-08-699-716A-2 x V41601 (1)
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Quality:
                                                                                                                                                                                                         seq_name: N_Geneseq_36:V41600
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Ratio: 4.255
Percent Similarity: 100.000
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                                       V41600;
26-OCT-1998 (first entry)
Nucleotide sequence of F1 antigen nYpF1mat474.
F1 antigen; plasmid; vaccine; plague; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haanes EJ, Osorio JE, Thomas RE;

WPI; 98-33331/29.

Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp.

Claim 8; Page 61; 75pp; English.

This is the nucleoride sequence of a Yersinia pestis F1 antigen, us in the method of the invention. Plasmid and host cells are uşed to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable oprotecting an animal from contracting plague.

Sequence 450 BP; 134 A; 102 C; 96 G; 118 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9824912-A2.
11-JUN-1998.
04-DEC-1997; U22617.
04-DEC-1996; US-767115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1998 (first entry)
Nucleotide sequence of F1 anti
F1 antigen; plasmid; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102
                                                                                                                                                                                                                                                                    145 KVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAAGKYTDAVTVTVSNQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pestis.
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                                   Location/Qualifiers
                   .459
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Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
ID 092817 standard: DNA;
AC 092817
DT 17-DEC-1995 (first e
DE yersinia pestis cafil
KW Vaccine: antigen; Sal
KW Vaccine: plague: pneum
OS yersinia pestis.
FT cds
FT misc_feature 1...
FT misc_feature 1...
FT misc_feature 536.
FT misc_feature 536.
FT misc_feature 536.
FT MSC_1994; GO2818.
PR 24-DEC-1993; GB-0264;
PA (MINA) UK SEC FOR DI
PI Howells A, Leary SER
WPI; 95-24639632.
PR WPI; 95-24639632.
DR constructs capab.
PT uesd as live or attel
PT against Yersinia pes:
PS Claim 7; Page 15-16;
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US-08-699-716A-2 x V41600
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04-DEC-1997; U22617.

04-DEC-1996; US-767115.

(HESK-) HESKA CORP.

Hannes EJ, OSOTIO JE, Thomas RE;

WPI; 98-333331/29.

P-PSDB: W59787
                                                                                       06-JUL-1995.
23-DEC-1994; G02818.
24-DEC-1993; GB-026425.
(MINA) UK SEC FOR DEFENCE.
HOWells A, Leary SEC, Oystom PI; 95-246396/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 8; Pages 59-60; 75pp; English.

This is the nuclectide sequence of a Yersinia pestis F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable of protecting an animal from contracting plague.

Sequence 474 BP; 143 A; 106 C; 99 G; 126 T;
   DNA constructs capable of transforming microorganisms - which can used a live or attenuated vaccines which induce an immune respons against Yersinia pestis, at mucosal surfaces. Claim 7; Page 15-16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1995 (first entry)
Yersinia pestis cafl (F1) antigen in plasmid pFGAL2a.
Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
bubonic plague; pneumonic plague; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADLTASTTATATLVEPARITLTYKEGAPITIMDNGNIDTELLVGTLTLGG
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: 4.255
: 100.000
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1. .6
/*tag= b
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536. .541
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 541 BP
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                                                                                                                                                                                                                         "vector pFGAL2a bases"
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                                                                                                              Oyston PCF,
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                              promoter fusion site"
                                                                                                                Titball RW,
                                                                                                                Williamson
                                  ms - which can be immune response,
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alignment_block:
US-08-699-716A-2 x Q92817 (2)
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents the plasmid pFGAL2a construct showing the fusion of the first few bases of beta-galactosidase in the vector with the Y. pestis cafl (FI) antigen minus its signal sequence and having a 5′ tail including a SacI restriction site, and up to the cafl AACC-3′ end with some vector bases. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated to the colonization of the colonization 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, at are parenterally and orally active vaccines offering protection against bubonic and pneumonic plague.

Sequence 541 BP; 163 A; 120 C; 111 G; 147 T;
151 Q 151
                                                                                   193 Q 193
                                                                                                                                                                      101
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                                                                                                                                                                                                              SPKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAAGKYTDAVTVTVSN
                                                                                                                                                                      SPKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAAGKYTDAVTVTVSN
                                                                                                                                                                                                                                                                                                                                         GGYKTGTTSTSVNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRDFDI
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6
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: 4.185
: 100.000
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Gaps: 0
Percent Identity: 98.013
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50
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